

# STIC Search Report Biotech-Chem Library

#### STIC Database Tracking Number: 115605

To: James Schultz Location: rem/2d18/2c18

Art Unit: 1635

Monday, March 08, 2004

Case Serial Number: 09/646651

From: Beverly Shears Location: Remsen Bldg.

**RM 1A54** 

Phone: 571-272-2528

beverly.shears@uspto.gov

Search Notes	7. 201	



### SEARCH REQUEST FORM

Requestor's Name:		Seri Nur			
Date:	Phone:		Art	Unit:	
amen that may have a cou	atement of scarch topic. Des ecial meaning. Give exampl te sequence. You may includ	les or relevent citations,	authors, keywords	s, etc., if known. For se	Define any equences,
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Total time:		N.A		SDC	
Number of Searches: _			cture	DAR	C/Questel
Number of Databases:	1		liographic	Othe	CEN

PTO-1590 (9-90)

09/646651 Page 1 8-9.10s 19 2 c/ Inters

NUMBER OF SEQUENCES:

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA: APPLICATION NUMBER: US 08/794,000 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DE96/01337
FILING DATE: 17-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195 25 992.0
PILING DATE: 17-JUL-1995
PILING DATE: 17-JUL-1995
PILING DATE: 18-AUG-1995
PILING DATE: 18-AUG-1995 FITTE OF INVENTION: RESU US-0 ; Se March 5, 2004, 10:31:00 ; Search time 182 Seconds
(without alignments)
488.027 Million cell updates/sec 1 TKLEDHLEGIINIFHQYSVR.....EFVVLVTDVLITAHDNIHKE GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. 6/ptodata/2/paa/US60\_COMB.pep: otal number of hits satisfying chosen parameters: 6019581 segs, 976053577 residues Listing first 45 summaries model BLOSUM62 Gapop 10.0 , Gapext 0.5 M protein - protein search, using sw Ost-processing: Minimum Match 0% Maximum Match 100% inimum DB seq length: 0 US-09-646-651C-1 467 itle: erfect score: coring table: atabase : earched: ednence: un on:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Metal-Containing Ribonucleotide Polypeptides

Description

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Query Match Length DB

Score

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23	3	71.1	92		958-053-2	24	
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26	m	71.1	92		030-937-2	23,	
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8 6	m	71.1	92		755-889-33	334	
6 6	സ	71.1	92		440-068-334	334	
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45	7		139	22	9-760-484-	equence 450,	
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Sequence	,	2, Application	PC/1	DES	501337		
GENERAL IN APPLICAN	ANT	KMATLON:					

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TYPE: PRT
ORGANISM: Unknown
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US-09-791-537-101828
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LENGTH: 91
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                                                                                                                                                                       ; Score 467; DB 1; Length 91; Pred. No. 1.8e-44; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bandman, olga
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
IITLE OF INVENTION: NOVEL HUMAN SI00 PROTEINS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                       61 DANQDEQUSFKEFVVLVTDVLITAHDNIHKE 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FASTSEW: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,913
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    5-08-759-913-5
Sequence 5, Application US/08759913
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                       100.0%;
100.0%;
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                   SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
TYPE: amino acid
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INFORMATION FOR SEQ ID NO:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                      TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
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STATE: CA
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MOLECULE TYPE:
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APPLICANT: Bionomix.

APPLICANT: Bobe, Derek

APPLICANT: Debe, Derek

APPLICANT: Danzer, Joseph

TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE

TITLE OF INVENTION: METHODS OF USE THEREOF

FILE REFERENCE: 261/210

CURRENT APPLICATION NUMBER: US/09/791,537

CURRENT APPLICATION DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 153055

SOFTWARE: Patentin version 3.0

SEQ ID NO 101828

LENGTH: 91
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                                                                                                                                                                                                                                                                                                                                  APPLICANT: KUDA. Eckehard

APPLICANT: KUAN, Eckehard

APPLICANT: KUAN, Eckehard

APPLICANT: Bunner, Herwig

ITILB OF INVENTION: METAL-CONTAINING RIBONUCLECTIDE POLYPEPTIDES

FILE REFERENCE: 206579

CURRENT APPLICATION NUMBER: US/09/646,651C

CURRENT FILING DATE: 1998-11-30

PRIOR FILING DATE: 1998-11-30

PRIOR FILING DATE: 1998-03-13

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin version 3.0
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100.0%; Pred. No. 1.8e-44;
iive 0; Mismatches 0;
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OTHER INFORMATION: Angiotropin-related protein
                                                                                                                                  61 DANODEQVSFKEFVVLVTDVLITAHDNIHKE 91
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                                                                                                                                                                                                                                                          Sequence 1, Application US/09646651C
GENERAL INFORMATION:
APPLICANT: Klesewetter, Stefan
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Matches 91; Conservative
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Best Local Similarity 100.
Matches 91; Conservative
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TYPE: PRT
ORGANISM: Unknown
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ORGANISM: Unknown
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TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTKDQGTIDKIFQNL 60
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APPLICANT: Seibt, Jorg-Volker
APPLICANT: Noll, Michaela
TITLE OF INVENTION: METAL-CONTAINING RIBONUCLEOTIDE POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.4%; Score 455; DB 11; Length 91; 97.8%; Pred. No. 4.1e-43; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                     Sequence 9, Application US/08761289
GENERAL INFORMATION:
APPLICANT: Ni, J., ET AL.
TITLE OF INVENTION: Human Chemotactic Cytokine I
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-506 (PF210)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFRAX: 201-994-1744
                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD
                                                                                    DANODEQUSFKEFUVLVTDVLITAHDNIHKE 91
                                                                                                                   DANODEOVSFKEFVVLVTDVLITAHDNIHKE 91
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM P8/2
COPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/761,289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: December 6, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/008387
FILING DATE: December 8, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 97.8
Matches 89; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
S-08-761-289-9
                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: ROSELAND
STATE: NEW JERSEY
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APPLICANT: Kiesewetter, Stefan
APPLICANT: Kiesewetter, Brigitte
APPLICANT: Roch-Pelster, Brigitte
APPLICANT: Brunner, Herwig
IIIILE OF INVENTION: METAL-CONTAINING RIBONUCLEOTIDE POLYPEPTIDES
FILE REFERENCE: 206579
CURRENT APPLICATION NUMBER: US/09/646,651A
CURRENT FILING DATE: 2000-09-13
PRIOR APLICATION NUMBER: PCT/EP98/07722
PRIOR FILING DATE: 1998-11-30
PRIOR FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.4%; Score 455; DB 20;
97.8%; Pred. No. 4.1e-43;
live 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Angiotropin-related protein US-09-646-264A-1
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COTHER INFORMATION: Angiotropin-related protein US-09-646-651A-1
CURRENT APPLICATION NUMBER: US/09/646,264A
CURRENT FILING DATE: 2010-05-07
PRIOR APPLICATION NUMBER: PCT/FP99/00834
PRIOR PILING DATE: 1999-02-09
PRIOR PPLICATION NUMBER: DE19810998.9
PRIOR PELING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 91
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Best Local Similarity 97.8<sup>3</sup>
Matches 89; Conservative
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US-09-167-705-3

Sequence 3, Application US/09167705B

Sequence 3, Application US/09167705B

GENERAL INFORMATION.

APPLICANT: Schemid, Ann Maxie

APPLICANT: Stern, David

TITLE OF INVENTION: Extracellular Novel RAGE Binding Protein (EN-RAGE) and

TITLE OF INVENTION: USes Thereof

FILE REFERENCE: 0575/55873

CURRENT APPLICATION NUMBER: US/09/167,705B

CURRENT FILING DATE: 1998-10-06
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4.7e-33;
ches 8; Indels
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APPLICANT: Harold, Kevan
APPLICANT: Yan, Shi Du
APPLICANT: Yan, Shi Du
APPLICANT: Schmidt, Ann Maxie
APPLICANT: Lamster, Ira
TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
FILE REFERENCE: 0575/64080
CURRENT APPLICATION NUMBER: US/09/872,185
CURRENT APPLICATION NUMBER: US/09/872,185
NUMBER OF SILIN OS: 16
SOFTWARE: Patentin version 3.1
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4.7e-33;
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APPLICANT: Stern, David M.
APPLICANT: Herold, Kevan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/09872185 GENERAL INFORMATION:
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81.1%;
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Best Local Similarity 81.1%;
Matches 73; Conservative
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Best Local Similarity 81.1
Matches 73; Conservative
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                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
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US-09-872-185-11
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERRICE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE ParentIn version 3.0
SEQ ID NO 99618
LENGTH: 92
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Sequence 1, Application US/09646651B

Sequence 1, Application US/09646651B

APPLICANT: Kiesewetter, Stefan

APPLICANT: Kuhn, Eckehard

APPLICANT: Kuhn, Eckehard

APPLICANT: Kuhn, Eckehard

APPLICANT: Whin, Eckehard

TITLE OF INVENTION: METAL-CONTAINING RIBONUCLEOTIDE POLYPEPTIDES

TITLE OF INVENTION: METAL-CONTAINING RIBONUCLEOTIDE POLYPEPTIDES

TITLE OF INVENTION NUMBER: US/09/646,651B

CURRENT APPLICATION NUMBER: DE 198 11 047.2

PRIOR FILING DATE: 1998-03-13

PRIOR FILING DATE: 1998-03-13

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin version 3.0

SEQ ID NO 1

LENGTH: 91
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Pred. No. 4.1e-43;
0; Mismatches 2;
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Pred. No. 1.3e-33;
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81.3%;
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Best Local Similarity 97.8%;
Matches 89; Conservative
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Best Local Similarity 81.3
Matches 74; Conservative
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US-09-791-537-99618
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ORGANISM: Unknown
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US-09-791-537-99618
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US-09-872-185B-12
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US-10-666-513-3
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Pred. No. 4.7e-33;
9; Mismatches 8; Indels
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APPLICANT: Herold, Kevan
APPLICANT: Herold, Kevan
APPLICANT: Schmidt, Kevan
APPLICANT: Schmidt, Ann Marie
APPLICANT: Lanster, Ira
TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
FILLE REFREENCE: 0575/64080
CURRENT APPLICATION NUMBER: US/09/872,185B
CURRENT FILING DATE: 2001-06-01
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 11
LENGTH: 90
                                   APPLICANT: Lamster, Ira
TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
FILE REPERBINE: 0575/64080
CURRENT APPLICATION NUMBER: US/09/872,185
CURRENT FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 90
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GENERAL INFORMATION:
APPLICANT: Stern, David M.
APPLICANT: Herold, Kevan
APPLICANT: Yan, Shi Du
APPLICANT: Schmidt, Ann Marie
APPLICANT: Lanster, Ira
APPLICANT: Lanster, Ira
ITILE OF INVENTION: METHODS FOR TREATING INFLAMMATION
FILE REFERENCE: 0575/64080
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Pred. No. 4.7e-33;
9; Mismatches 8;
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81.1%;
Yan, Shi Du
Schmidt, Ann Marie
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ilarity 81.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                   73; Conservative
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Best Local Similarity
Matches 73; Conserv
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Best Local Similarity
Matches 73; Conserv
                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Bovine
S-09-872-185-12
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ORGANISM: Bovine
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APPLICANT: Stern, David
APPLICANT: Stern, David
TITLE OF INVENTION: Extracellular Novel RAGE Binding Protein (EN-RAGE)
TITLE OF INVENTION: Uses Thereof
TITLE OF INVENTION: 0575/55873
CURRENT APPLICATION NUMBER: US/10/666,513
CURRENT FILING DATE: 2003-09-19
PRIOR FILING DATE: 1998-110-06
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTING DATE: 1998-110-06
NUMBER OF SEQ ID NOS: 5
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                                                                                                                                                                                                                                        78.4%; Score 366; DB 23;
81.1%; Pred. No. 4.7e-33;
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Pred. No. 4.7e-33;
                                                                                                                                                                                                                                                                                      9; Mismatches
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CURRENT APPLICATION NUMBER: US/09/872,185B
CURRENT FILING DATE: 2001-06-01
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
SEQ ID NO 12
LENGTH: 90
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81.1%;
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Best Local Similarity 81.1
Matches 73; Conservative
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Best Local Similarity
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US-10-665-867-3
; Sequence 3, Application US/10665867
; GENERAL INFORMATION:
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; ORGANISM: Bovine
US-10-665-867-3
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Best Local Simi
Matches 73;
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LENGTH: 90
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178, App
10, Appl
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39009, A
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Appl
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Sequence 40040, A
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2, Appli
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                                                             March 5, 2004, 10:31:35; Search time 10 Seconds (without alignments) 91.517 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 32,
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'G972 6/ptodata/1/paa/USO6 NBW COMB.pep:*

'G972 6/ptodata/1/paa/USO6 NBW COMB.pep:*

'G972 6/ptodata/1/paa/USO8 NBW COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-624-631-31

US-10-624-631-31

US-10-624-631-29

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US-10-624-631-29

US-10-624-631-39

US-10-624-631-39

US-10-624-631-34

US-10-624-631-34

US-10-624-631-34

US-10-624-631-39

US-10-624-631-39

US-10-624-631-39

US-10-624-631-39

US-10-624-631-39

US-10-624-631-39

US-10-767-701-38583

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US-10-767-701-39099
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Maximum Match 1008
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match Length DB
                                           protein search,
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498
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61992, A	5555, Ap	40255, A	49565, A	506, App	505, App	38, Appl	38434, A	224, App	4239, Ap	37, Appl	37, Appl	4910, Ap	4912, Ap	5050, Ap	57231, A	4507, Ap	38,	3995, Ap
Sequence 6	Sequence 5	Sequence 4	Sequence 4	Seguence 5	Sequence 5						Sequence 3	Sequence 4	Sequence 4	Sequence 5		Seguence 4	Sequence 45	Seguence 3
US-10-767-701-61992	US-10-417-884A-5555	US-10-767-701-40255	US-10-767-701-49565	US-09-830-230A-506	US-09-830-230A-505	US-10-416-330-38	US-10-767-701-38434	US-10-451-467A-224	US-10-417-884A-4239	PCT-US04-03291-37	US-10-771-931-37	US-10-417-884A-4910	US-10-417-884A-4912	US-10-417-884A-5050	US-10-767-701-57231	US-10-417-884A-4507	US-10-417-884A-4508	US-10-417-884A-3995
198 6				44 5								319 6					42 6	255 6
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64.5	64.5	64	63.5	63.5	63.5	62	61.5	61.5	61	61	61	60.5	60.5	9	59.5	59.5	59.5	59.5
27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

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SERVICAN; Schmid, A. Min Marie
APPLICANT: SOND-09-10-10
PRING PILING DATE: 2003-09-10
PRING PILING DATE: 2003-09-10
PRING PILING DATE: 2001-09-10
PRING PILING DATE: 2001-
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APPLICANT: Grasso, Luigi
APPLICANT: Kline, J. Bradford
APPLICANT: Nicolaides, Nicholas C.
APPLICANT: Sass, Philip M.
TILLE OF INVENTION: Methods for Generating Enhanced Antibody-Producing Cell Lines wit
TILLE OF INVENTION: Improved Growth Characteristics
TILLE OF INVENTION: Improved Growth Characteristics
CURRENT APPLICATION: 12002-07-21
CURRENT PAPLICATION NUMBER: 60/397,027
PRIOR PILING DATE: 2002-07-19
PRIOR FILING DATE: 2002-07-19
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APPLICANT: Kline, J. Bradford
APPLICANT: Nicolaides, Micholae C.
APPLICANT: No Sass, Micholae C.
APPLICANT: Sass, Philip M.
TITLE OF INVENTION: Methods for Generating Enhanced Antibody-Producing Cell Lines wit
FILE REFERENCE: MOR-0241/HD0002 US
CURRENT APPLICATION NUMBER: US/10/624,631
CURRENT FILING DATE: 2003-07-21
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                                                                      Gaps
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                                                                      Indels
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35.2%; Pred. No. 3.2e-10;
tive 24; Mismatches 31
                          Score 159; DB 6;
Pred. No. 3.9e-11;
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                                                                      23; Mismatches
                                                                                                                                                                                                             61 DANQDEQVSFKEFVVLVTDVLITAHDNIHKE 91
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PRIOR FILING DATE: 2002-07-19
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.1
SEQ ID NO 28
LENGTH: 98
                                                                                                                                                                                                                                                                                                                                                  5-10-624-631-31
Sequence 31, Application US/10624631
GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Morphotek, Inc.
                     34.0%;
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SOFTWARE: Patentin version 3.1
SEQ ID NO 31
LENGTH: 93
                                                                      30; Conservative
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Best Local Similarity 35.2
Matches 32; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-624-631-31
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                          Query Match
Best Local Similarity
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APPLICANT: Schmidt, Ann Marie
APPLICANT: Schmidt, David
TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE
FILE REFERENCE: 0575/55873-B-PCT-US
CURRENT APPLICATION NUMBER: US/10/665,867
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: US/09/826,589
PRIOR FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 50
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APPLICANT: Grasso, Luigi
APPLICANT: Kine, J. Bradford
APPLICANT: Nicolaides, Nicholas C.
APPLICANT: Nicolaides, Nicholas C.
APPLICANT: Sass, Philip M.
TITLE OF INVENTION: Methods for Generating Enhanced Antibody-Producing Cell Lines wit
TITLE OF INVENTION: Improved Growth Characteristics
FILE REPERENCE: MOR-0241/H00002 US
CURRENT APPLICATION NUMBER: US/10/624,631
CURRENT FILING DATE: 2003-07-21
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                                                                                                                                      8; Indels
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                                                                                            Score 366; DB 6;
Pred. No. 3.6e-34;
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Pred. No. 1e-16;
3; Mismatches
                                                                                                                                      9; Mismatches
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                                                                                                                                                                                                                                                                             61 DANQDEQUSFKEFUVLVTDVLITAHDNIHK 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (47)...(47)
; OTHER INFORMATION: x=any amino acid
US-10-665-867-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/397,027
PRIOR FILING DATE: 2002-07-19
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.1
LENGTH: 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 32, Application US/10624631
GENERAL INFORMATION:
APPLICANT: Morphotek, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                               US-10-665-867-2; Sequence 2, Application US/10665867; GENERAL INFORMATION:
                                                                                     78.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       th 44.1%; l Similarity 82.0%; 41; Conservative
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                                                                                                                                      73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MISC FEATURE
                                                                                       Query Match
Best Local Similarity
Matches 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 41; Conserv
TYPE: PRT
ORGANISM: Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JS-10-624-631-32
                                            US-10-665-867-4
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APPLICANT: Grasso, Luigi
APPLICANT: Kline, J. Bradford
APPLICANT: Nicolaides, Nicholas C.
APPLICANT: Sass, Philip M.
TITLE OF INVENTION: Methods for Generating Enhanced Antibody-Producing Cell Lines wit
TITLE OF INVENTION: Improved Growth Characteristics
FILE REPERBNCE: MOR-0241/HD0002 US
                                                                                                                                                                                                                                4 LIAVPQKFAGKEGNNCTLSKTEFLTFMNTELAAFTKNOKDPGVLDRYMKKLDLNSDGQLD
                                                                                                                                                                                                  10 IINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTKDQGTIDKIFQNLDANQDEQVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kenji OKUSE
APPLICANT: Mark BAKER
APPLICANT: Louis POON
APPLICANT: Jouns POON
APPLICANT: John ALIAN-HALL
TITLE OF INVENTION: SODIUM CHANNEL REGULATORS AND MODULATORS
FILE REPERRENCE: 117-492 / N. 86242A GCW
CURRENT APPLICATION NUMBER: US/10/487,337
CURRENT APPLICATION DATE: 2004-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.5%; Score 133; DB 6; Length 99; 32.2%; Pred. No. 3.6e-08;
                                                                                                                                                    33; Indels
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                                                                                               28.7%; Score 134; DB 6;
34.6%; Pred. No. 2.4e-08;
tive 18; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 DANQDEQVSFKEFVVLVTDVLITAHDNIHK 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/624,631
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: 60/397,027
PRIOR FILING DATE: 2002-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2004-02-20
PRIOR APPLICATION NUMBER: PCT/GB02/03852
PRIOR FILING DATE: 2002-08-20
PRIOR APPLICATION NUMBER: GB 0120238.1
PRIOR FILING DATE: 2001-08-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 33, Application US/10624631; GENERAL INFORMATION: APPLICANT: Morphotek, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-487-337-8; Sequence 8, Application US/10487337; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                  70 FKEFVVLVTDVLITAHDN 87
                                                                                                                                                                                                                                                                                                                             |:||: |: | ||:
64 FQEFINLIGGMAIACHDS 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin version 3.1 SEQ ID NO 33 LENGTH: 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn version 3.1
                                                                                               Query Match
Best Local Similarity 34.6'
Matches 27; Conservative
                           ORGANISM: Canis familiaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                   ; US-10-624-631-29
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  TYPE: PRT
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APPLICANT: Grasso, Luigi
APPLICANT: Grasso, Luigi
APPLICANT: Nicolaides, Nicolaides
APPLICANT: Nicolaides, Nicolaides
APPLICANT: Nicolaides, Nicolaides
APPLICANT: Sass, Philip M.
APPLICANT: Sass, Philip M.
TITLE OF INVENTION: Methods for Generating Enhanced Antibody-Producing Cell Lines wit
TITLE OF INVENTION: MORER: US/10/624,631
CURRENT APPLICATION NUMBER: US/10/624,631
CURRENT FILING DATE: 2003-07-21
PRIOR FILING DATE: 2002-07-19
NUMBER OF SEQ ID NOS: 34
SEQ ID NO 29
LENGTH: 90
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                                                                                                                                               TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTKDQGTIDKIFQNL 60
                                                                                                                                                                              |: | : | : | : | : | : | : | : | THETERCIESLIANFELAAFTKNOKDPGVLDRMMKKL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTKDQGTIDKIFQNL 60
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                                                                                                    Gaps
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GENERAL INFORMATION:
APPLICANT: Kenji OKUSE
APPLICANT: Acnji OKUSE
APPLICANT: MISHA BAKER
APPLICANT: John Nicholas WODN
APPLICANT: John Nicholas WODN
APPLICANT: Mishah MALIK-HALL
TITLE OF INVENTION: SOULUM GHANNEL REGULATORS
FILE REFERENCE: 117-492 / N 86242A GCW
CURRENT FILING DATE: 2004-02-20
PRIOR APPLICATION NUMBER: PCT/GB02/03852
PRIOR FILING DATE: 2004-02-20
PRIOR APPLICATION NUMBER: GB 0120238.1
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PATCHING DATE: 2010-08-20
NUMBER OF SEQ ID NOS: 55
SEQ ID NO 4
LENTH: 95
LENTH: 95
LENTH: 95
LENTH: 95
LENTH: 95
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                                                  Length 98;
                                                                                               Indels
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                                               31.3%; Score 146; DB 6; 35.6%; Pred. No. 1.3e-09;
                                                                                               18; Mismatches
                                                                                                                                                                                                                                               87
                                                                                                                                                                                                                                                                           63 DLNCDGQLDFQEFLNLIGGLAIACHDS 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | : | : | : | : | : | : | 60 DQCRDGKVGFQSFLSLVAGLIIACND 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 DANQDEQVSFKEFVVLVTDVLITAHD 86
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 32.6
Matches 28; Conservative
                                                                                               Conservative
                                               Query Match
Best Local Similarity
                                                                                             31;
IS-10-624-631-28
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IS-10-624-631-29
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                                                                                               Matches
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Gaps

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APPLICANT: Grasso, Luigi
APPLICANT: Kline, J. Bradford
APPLICANT: Kline, J. Bradford
APPLICANT: Nicolaides, Micholas C.
APPLICANT: Sass, Philip M.
TITLE OF INVENTION: Methods for Generating Enhanced Antibody-Producing Cell Lines wit
TITLE OF INVENTION: Improved Growth Characteristics
TITLE OF INVENTION: Improved Growth Characteristics
CURRENT APPLICATION NUMBER: US(10/624,631
CURRENT PILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: 60/397,027
PRIOR FILING DATE: 2002-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bayer Pharmaceuticals Corporation
APPLICANT: Breleigh, Deepa
APPLICANT: Breleigh, Deepa
APPLICANT: Breleigh, Deepa
APPLICANT: Breleigh, Deepa
APPLICANT: Taylor, Ian
TITLE OF INVENTION: EXPRESSION PROFILES FOR COLON CANCER AND METHODS OF USE
FILE REFERENCE: 5151
CURRENT PELLING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: 60/442,582
PRIOR APPLICATION NUMBER: 60/442,582
NUMBER OF SEQ ID NOS: 191
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                3 QLLQNINGIIEAFRRYARTEGNCTALTRGELKRLLEQEFADVIVKPHDPATVDEVLRLLD 62
                                                                                                                                                                                                  2 KLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTKDQGTIDKIFQNLD 61
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                                                                                                                                                Gaps
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                                                                                   Query Match

26.6%; Score 124; DB 6; Length 495;
Best Local Similarity 34.2%; Pred. No. 3.5e-06;
Matches 27; Conservative 18; Mismatches 34; Indels
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23.3%; Score 109; DB 6;
Best Local Similarity 37.3%; Pred. No. 8.4e-06;
Matches 22; Conservative 11; Mismatches 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 30, Application US/10624631
                                                                                                                                                                                                                                                                                                        62 ANODEQUSEKEEVVLVTDV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                             63 EDHTGTVEFKEFLVLVFKV
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36.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.1
        , ORGANISM: Homo sapiens
US-10-767-471-717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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LENGTH: 104
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ORGANISM:
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APPLICANT: Kline, J. Bradford
APPLICANT: Kline, J. Bradford
APPLICANT: Kline, J. Bradford
APPLICANT: Nicolaides, Nicholas C.
APPLICANT: Sass, Philip M.
TITLE OF INVENTION: Improved Growth Characteristics
TITLE OF INVENTION: Improved Growth Characteristics
CURRENT APPLICATION NUMBER: US/10/624,631
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: 60/397,027
PRIOR APPLICATION NUMBER: 60/397,027
PRIOR APPLICATION NUMBER: 50/307-19
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.1
LENGTH: 88
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS, METHODS OF DETECTION AND USES THEREOF
FILER REPERENCE: CLOOLSOS
FILER REPERENCE: CLOOLSOS
FULER REPERENCE: CLOOLSOS
CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT APPLICATION NOWHER: US/10/767,471
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 717
LENGTH: 495
                                                                                                                                                                                                                                                                    1 TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTKDQGTIDKIFQNL 60
                                                                                                                                                                                                                                                                                                        3 SQMEHAMETHWRETFHKFAGDKGY---LTKEDLRVLMEKEFPGFLENQKDPLAVDKIMKDL 59
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                                                                                                                                                                                                                        Gaps
                                                                                                                                                                   Length 97;
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                                                                                                                                                              ; Score 129.5; DB 6; Pred. No. 8.5e-08; 23; Mismatches 32
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27.2%; Score 127; DB 6;

Best Local Similarity 34.6%; Pred. No. 1.4e-07;

Matches 27; Conservative 17; Mismatches 32.
                                                                                                                                                                                                                                                                                                                                                                                                                 60 DOCRDGKVGFOSFFSLIAGLTIACND 85
                                                                                                                                                                                                                                                                                                                                                                                61 DANQDEQVSFKEFVVLVTDVLITAHD 86
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CTHER INFORMATION: Consensus Sequence

US-10-624-631-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 34, Application US/10624631
GENERAL INFORMATION:
APPLICANT: Morphotek, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 FKEFUVLVTDVLITAHDN 87
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66 FOEFLNLIGGLAIACHDS 83
                                                                                                                                                              32.6%;
                                                                                                                                                           Query Match 27.7% (Best Local Similarity 32.6% Matches 28; Conservative
                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-767-471-717
                                                                                                         US-10-487-337-8
SEQ ID NO 8
LENGIH: 97
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27; Conservative 18; Mismatches 26; Indels

Matches

earch completed: March 5, 2004, 10:39:30 ob time: 10 secs

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| cgn2_6/ptodata/2/pna/US08_COMB.seq:*
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                      GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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OTHER INFORMATION: N is nucleotide A, C,
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OTHER INFORMATION: Synthetic
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TYPE: RNA
ORGANISM: Artificial
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APPLICANT: Kaesewetter, Stefan
APPLICANT: Kach-Pelster, Brigitte
APPLICANT: Koch-Pelster, Brigitte
APPLICANT: Brunner, Herwig
TITLE OF INVENTION: METAL-CONTAINING RIBONUCLEOTIDE POLYPEPTIDES
TITLE REFERENCE: 206579
CURRENT APPLICATION UNMBER: DCT/EP98/07722
PRIOR APPLICATION NUMBER: PCT/EP98/07722
PRIOR APPLICATION NUMBER: DE 198 11 047.2
PRIOR APPLICATION NUMBER: DE 198 11 047.2
PRIOR PILING DATE: 1998-01-13
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NAME/KEY: misc feature
LOCATION: (73)...(73)
OTHER INFORMATION: N is
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LOCATION: (74)..(74)
OTHER INFORMATION: N is
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ORGANISM: Artificial
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OTHER INFORMATION: N is nucleotide A,
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STHER INFORMATION: N is nucleotide A,
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OTHER INFORMATION: N is nucleotide A,
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LOCATION: (57) ... (57)
DTHER INFORMATION: N is nucleotide A,
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LOCATION: (58)...(58)
JTHER INFORMATION: N is nucleotide A,
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LOCATION: (66)...(66)
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LOCATION: (67)...(67)
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THER INFORMATION: N is nucleotide A,
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LOCATION: (39)...(39)
DTHER INFORMATION: N is nucleotide
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LOCATION: (59)...(59)
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LOCATION: (9)...(9)
OTHER INFORMATION: N is nucleotide A,
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LOCATION: (14)...(14)
OTHER INFORMATION: N is nucleotide A,
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INFORMATION: N is nucleotide A,
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OTHER INFORMATION: N is nucleotide A,
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OCATION: (25)...(25)
THER INFORMATION: N is nucleotide A,
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JHER INFORMATION: N is nucleotide A,
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LOCATION: (34)...(34)
DTHER INFORMATION: N is nucleotide A,
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THER INFORMATION: N is nucleotide A,
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OCATION: (29)...(29)
THER INFORMATION: N is nucleotide
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THER INFORMATION: N is nucleotide
FEATURE:
OTHER INFORMATION: Synthetic
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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LOCATION: (36)..(36)
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GYNERAL INFORMATION:
APPLICANT: Kiesewetter, Stefan
APPLICANT: Koch-Pelster, Brigitte
APPLICANT: Koch-Pelster, Brigitte
APPLICANT: Brunner, Herwig
TILLE OF INVENTION: METAL-CONTAINING RIBONUCLEOTIDE POLYPEPTIDES
FILE REPERENCE: 206579
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APPLICANT: Roch-Pelster, Brigitte
APPLICANT: Brunner, Herwig
TITLE OF INVENTION: METAL-CONTAINING RIBONUCLECTIDE POLYPEPTIDES
FILE REFERENCE: 206579 TEAL-CONTAINING RIBONUCLECTIDE POLYPEPTIDES
CURRENT PELING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: PCT/EP98/C7722
PRIOR APPLICATION NUMBER: DE 198 11 047.2
PRIOR PILING DATE: 1998-03-13
                                              Length 298;
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                                              DB 27;
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Pred. No. 58;
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                                            Score 31.4; I
Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/646,651B CURRENT FILING DATE: 2000-09-13 PRIOR APPLICATION NUMBER: PCT/EP98/07722 PRIOR FILING DATE: 1998-11-30 PRIOR FILING DATE: 1998-11-30 PRIOR FILING DATE: 1998-03-13 PRIOR FILING DATE: 1998-03-13 SUMBER: PEC SEQ ID NOS: 4 SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09646651C GENERAL INFORMATION:
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                                           29.3%;
ilarity 42.1%;
Conservative
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1 Similarity 42.1%;
32; Conservative
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OTHER INFORMATION: SDRNA
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NAME/KEY: misc feature
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LENGTH: 298
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APPLICANT: Koch-Pelster, Brigitte
APPLICANT: Koch-Pelster, Brigitte
APPLICANT: Brumer, Herwig
TITLE OF INVENTION: METAL-CONTAINING RIBONUCLEOTIDE POLYPEPTIDES
FILE REFERENCE: 206579
CURRENT APPLICATION NUMBER: DC/8P98/07722
PRIOR FILING DATE: 2090-09-13
PRIOR FILING DATE: 1998-11-30
PRIOR FILING DATE: 1998-13-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
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LOCATION: (86)...(86)
OTHER INFORMATION: N is nucleotide A,
                           LOCATION: (73)...(73)
OTHER INFORMATION: N is nucleotide A,
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LOCATION: (85)...(85)
OTHER INFORMATION: N is nucleotide A,
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LOCATION: (74)...(74)
OTHER INFORMATION: N is nucleotide A,
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OTHER INFORMATION: N is nucleotide A,
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OTHER INFORMATION: N is nucleotide A,
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OTHER INFORMATION: N is nucleotide A,
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APPLICANT: Kuhn, Eckehard
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Best Local Similarity 100.
Matches 107; Conservative
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OTHER INFORMATION: N is
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NAME/KEY: misc_feature
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us-09-646-651c-2.rnpm

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APPLICANT: Bult et al.

APPLICANT: Bult et al.

TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ

TITLE OF INVENTION: jannaschii

FILE OF INVENTION: jannaschii

FILE SEFERENCE: PB275C1

CURRENT APPLICATION NUMBER: US/09/692,570

FILE REPERENCE: DATE: 2003-01-14

FRIOR PELING DATE: 1996-08-22

FRIOR FILING DATE: 1996-08-22

PRIOR FILING DATE: 1997-08-22

NUMBER: OF SEQ ID NOS: 20
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                                                                                                                                                          APPLICANT: Venter, J. Craig
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic
TITLE OF INVENTION: Archaeon, Methanococcus jannaschii
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  DEPARTMENT OF MOLECULAR BIOLOGY AND GENETICS BALLTHORE, MD 21205
BALTHORE, AD 21205
BALTHORE STATES OF AMERICA
APPLICANTS/INVENTORS: Bult, Carol J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US97/14900A FILING DATE: 22-AUG-1997
                                                                                                                                                                                                                                                                      ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX STREET: 1100 New York Avenue, NW, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.5%; Score 29.4; DB: 24.8%; Pred. No. 2e+03; Cive 10; Mismatches (
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CLASSIFCCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,428
FILING DATE: 22-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bric K. Steffe
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 36,688
                                                                                         White, Owen R.
Smith, Hamilton O.
Woese, Carl R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1664976 base pairs
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STRANDEDNESS: double
                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20005-3934
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                    WASHINGTON
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US-09-692-570-1/c
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STATE: DO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90594 GGAAACATCTATTAATTTGTGACTTTTTACATTGCCCAGAAATTTGTAAGCATGGTCTC 90653
                                                                                                                                                                                                                                                                                                                                                                                                     89 UUUGUACAUAAAAUAAAAAAAAAAAGACOUCUUUAGACACUCCUUCAUUAGAAAUAAAAAAA 148
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                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                      Length 298;
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UNITED STATES OF AMERICA
SCHOOL OF MEDICINE
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ROCKVILLE, MD 20850
UNITED STATES OF AMERICA
MICROBIOLOGY DEPARTMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JS-60-466-412-84605
; Sequence 84605
; General INFORMATION:
APPLICANT: CARGILL, Michele
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NAME/KEY: misc feature
LOCATION: (1) ... (226307)
OTHER INFORMATION: n = A,T,C or G
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NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
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OTHER INFORMATION: SDRNA
JS-09-646-651C-4
                                                                                                                              FEATURE:
NAME/KEY: misc feature
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                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                       TYPE: RNA
ORGANISM: Unknown
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LOCATION: (234187)...(234187)
OTHER INFORMATION: n equals a, t, c,
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                                             TYPE: DNA ORGANISM: Methanococcus jannaschii
                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: misc_feature
LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals a, t,
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NAME/KEY: misc feature
LOCATION: (98120). (98120)
OTHER INFORMATION: n equals a, t,
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NAME/KEY: misc_feature
LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals a, t,
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LOCATION: (98239)..(98239)
OTHER INFORMATION: n equals a, t,
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NAME/KEY: misc_feature
LOCATION: (98266)..(98266)
OTHER INFORMATION: n equals a, t,
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NAME/KEY: misc_feature
LCOATION: (98343)
OTHER INFORMATION: n equals a, t,
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LOCATION: (103998)..(103998)
OTHER INFORMATION: n equals a, t,
FEATURE:
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LOCATION: (148948)..(148948)
OTHER INFORMATION: n equals a, t,
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LOCATION: (163385)..(163385)
OTHER INFORMATION: n equals a, t,
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LOCATION: (191989)..(191989)
OTHER INFORMATION: n equals a, t,
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LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals a, t,
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LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals a, t,
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LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals a, t,
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LOCATION: (191995)..(191995)
OTHER INFORMATION: n equals a, t,
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NAME/KEY: misc_feature
LOCATION: (28222)
OTHER INFORMATION: n equals a,
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LOCATION: (231980)..(231980)
OTHER INFORMATION: n equals a,
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 1664976
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LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals a, t,
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NAME/KEY: misc_feature
LOCATION: (559241)..(559241)
OTHER INPORMATION: n equals a,
NAME/KEY: misc feature
LOCATION: (234220)..(234220)
OTHER INFORMATION: n equals a,
                                                                                                             NAME/KEY: misc feature
LOCATION: (309398)..(309398)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (312837)..(312837)
OTHER INFORMATION: n equals a,
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LOCATION: (319226)..(319226)
OTHER INFORMATION: n equals a,
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LOCATION: (600992)..(600992)
OTHER INFORMATION: n equals a,
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LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals a,
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LOCATION: (682442)..(682442)
OTHER INFORMATION: n equals a,
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LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals a,
                                                       NAME/KEY: misc feature
LOCATION: (234814)..(234814)
OTHER INFORMATION: n equals a,
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NAME/KEX: misc_feature
LOCATION: (309418).(309418)
OTHER INFORMATION: n equals a,
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LOCATION: (312993)..(312993)
OTHER INFORMATION: n equals a,
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LOCATION: (559167)..(559167)
OTHER INFORMATION: n equals a,
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LOCATION: (657203)..(657203)
OTHER INFORMATION: n equals a,
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LOCATION: (674435)..(674435)
OTHER INFORMATION: n equals a,
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LOCATION: (713652)..(713652)
OTHER INFORMATION: n equals a,
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NAME/KEY: misc_feature
LOCATION: (657081)..(657081)
OTHER INFORMATION: n equals a,
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                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kerlavage, Anthony
TITLE OF INVENTION: ISOLATED KINASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES ENCODING KINASE PROTEINS, AND USES THEREOF
FILE REFERENCE: CLO00038
CURRENT APPLICATION NUMBER: US/60/140,806
CURRENT FILING DATE: 1999-06-25
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 255, Application US/60141856
GENERAL INFORMATION:
APPLICANT: Kerlavage, Anthony
TITLE OF INVENTION: ISOLATED KINASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: ISOLATED KINASE PROTEINS, AND USES THEREOF
FILE REFERENCE: CL000044
CURRENT APPLICATION NUMBER: US/60/141,856
CURRENT FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 617
SOFTWARE: FastSEQ for Windows Version 3.0
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                609;
              Length
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                                                      Indels
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            DB 69;
            27.3%; Score 29.2; DB 69
25.0%; Pred. No. 2.9e+02;
rative 13; Mismatches 50
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25.0%; Pred. No. 3.2e+02;
iive 13; Mismatches 50
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                                                                                                                                                                                                                                                                                                          Sequence 338, Application US/60140806 GENERAL INFORMATION:
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27.3%;
Best Local Similarity 25.0%;
Matches 21; Conservative
                                                    21; Conservative
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            Query Match
Best Local Similarity
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ORGANISM: Drosophila
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Best Local Similarity
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US-60-141-856-255
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LENGTH: 2334
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LENGIH: 903
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kerlawage, Anthony
TITLE OF INVENTION: ISOLATED KINASE PROTEINS, AND USES THEREOF
FILLS REPRENCE: CLO00028
CURRENT APPLICATION NUMBER: US/60/138,831
CURRENT FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 620
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 96
LENGTH: 609
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LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a, t,
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                                                                                    NAME/KEY: misc feature
LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a,
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LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals a,
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LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a,
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LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a,
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LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a,
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LOCATION: (1096846)
OTHER INFORMATION: n equals a,
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LOCATION: (1130881)..(1130881)
OTHER INFORMATION: n equals a,
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LOCATION: (1313224)..(1313224)
OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
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Best Local Similarity 24.8%
Matches 26; Conservative
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; ORGANISM: Drosophila US-60-138-831-96

TYPE: DNA

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61 UUNAGNINININININININIAGAAAU 84

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TYPE: DNA ORGANISM: DROSOPHILA
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US-60-142-844-270
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Best Local Similarity
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GENERAL INFORMATION:
APPLICANT: Li, Peter, W.D.
TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING ISOLATED DROSOPHILA PROTEINS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Venter, J. Craig
APPLICANT: Venter, J. Craig
TITLE OF INVENTION: NUCLEIC ACID DETECTION KITS COMPRISING
TITLE OF INVENTION: GENE SEQUENCES EXPRESSED FROM THE DROSOPHILA GENOME, AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000392
CURRENT APPLICATION NUMBER: US/60/191,637
CURRENT FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 42660
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25467
LENGTH: 3020
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    Sequence 20990, Application US/60173464
GENERAL INFORMATION:
APPLICANT: Li, Peter W.D.
TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
TITLE OF INVENTION: THEREOF
FILE REFREENCE: CLOOD173
CURRENT APPLICANT: 1999-12-29
NUMBER OF SEQ ID NOS: 30269
SOFTWARE: FEQ ID NOS: 30269
SOFTWARE: FEASTER OF WINDOWN VERSION 4.0
SEQ ID NO 20990
LENGTH: 3020
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829 TTAATTTTAAATTCAAATTTAAAT 852
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829 TTAATTTTAAATTCAAATTTAAAT 852
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Sequence 25467, Application US/60191637
GENERAL INFORMATION:
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Best Local Similarity 25.05
Matches 21; Conservative
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Best Local Similarity
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S-60-191-637-25467
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S-60-173-464-20990
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Sequence 270. Application US/60142844

GENERAL INFORMATION:
APPLICANT: Kerlavage, Anthony
TITLE OF INVENTION: MOLECULES ENCODING KINASE PROTEINS, AND USES THEREOF
TITLE OF INVENTION: MOLECULES ENCODING KINASE PROTEINS, AND USES THEREOF
FILE REPERENCE: CL000049
CURRENT APPLICATION NUMBER: US/60/142,844
CURRENT FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 730
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 270
LENGTH: 3238
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27.3%; Score 29.2; DB 70;
Best Local Similarity 25.0%; Pred. No. 4.5e+02;
Matches 21; Conservative 13; Mismatches 50;
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25.0%; Pred. No. 4.5e+02;
iive 13; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                        13; Mismatches
TITLE OF INVENTION: USES THEREOF.
FILE REFERENCE: cl000390
CURRENT APPLICATION NUMBER: US/60/191,681
CURRENT FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 30973
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20076
LENGTH: 3020
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829 TTAATTTTAAATTCAAATTAAAT 852
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2 GAAAAUNNNNNAUAUGNNNNNNNCUNNNJUUNNNNNNAAAAANUANAAAACAUNNNNNCU
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LOCATION: 479, 484, 486, 487, 496,
LOCATION: 515, 515, 521, 523
OTHER INFORMATION: n = A,T,C or G
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Sequence 172, App
Sequence 10627, A
Sequence 14, Appl
Sequence 10732, A
Sequence 8, Appli
Sequence 324, Appli
Sequence 324, Appli
Sequence 324, Appli
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Sequence 10612, A
Sequence 10702, A
Sequence 197, App
Sequence 10741, Ap
Sequence 10854, A
Sequence 10866, A
Sequence 10806, A
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Sequence 22493, A
Sequence 22418, A
Sequence 22415, A
Sequence 23307, A
Sequence 126, App
Sequence 10805, A
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Sequence 10805, A
Sequence 30635, A
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2: /cgn2 6/ptodata/2/pna/USOF_NEW_COMB.seg:*

3: /cgn2 6/ptodata/2/pna/USOR_NEW_COMB.seg:*

4: /cgn2 6/ptodata/2/pna/USOB_NEW_COMB.seg:*

5: /cgn2 6/ptodata/2/pna/USOB_NEW_COMB.seg:*

6: /cgn2 6/ptodata/2/pna/USOB_NEW_COMB.seg:*

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7: /cgn2 6/ptodata/2/pna/USOB_NEW_COMB.seg:*
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PCT-US04-02000-361
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US-10-767-471-10627
US-10-673-523-14
US-10-767-471-10732
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10844, A
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10823, A
10823, A
1919, Ap
22233, A
222331, A
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Sequence 10650, A
Sequence 10703, A
Sequence 10700, A
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APPLICANT; Williams et al
TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II
FILE REFERENCE: 2300-21302
CURRENT PILING DATE: 2004-02-12
PRIOR PILING DATE: 2004-02-15
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1998-04-03
PRIOR FILING DATE: 1998-04-04
PRIOR FILING DATE: 2000-04-10
PRIOR FILING DATE: 2000-04-10
PRIOR FILING DATE: 2000-04-10
PRIOR FILING DATE: 2000-04-10
PRIOR FILING DATE: 1998-01-28
PRIOR FILING DATE: 1998-01-28
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PRIOR FILING DATE: 1998-01-38
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PRIOR FILING DATE: 1998-01-38
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PRIOR FILING DATE: 1998-02-34
PRIOR FILING DATE: 1998-03-31
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US-10-417-375A-4

US-10-765-790-12

US-10-765-790-30

US-10-76-71-10844

US-10-76-71-10844

US-10-76-771-10823

US-10-76-771-10823

US-10-76-771-10823

US-10-76-771-10823

US-10-76-7471-10823

US-10-779-543-2015

US-10-779-543-22233

US-10-779-543-22331
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US-10-767-471-10700
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CURRENT APPLICATION NUMBER: US/10/779,543
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ORGANISM: Homo sapiens
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APPLICANT: Williams et al

TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED

TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED

TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II
FILE REFERENCE: 2300-21302

CURRENT APPLICATION NUMBER: US/10/779,543

CURRENT FILING DATE: 2004-02-12

PRIOR FILING DATE: 1994-12-21

PRIOR FILING DATE: 1996-12-21

PRIOR FILING DATE: 1996-12-23

PRIOR FILING DATE: 1998-4-03

PRIOR FILING DATE: 1998-4-04

PRIOR FILING DATE: 1998-4-02

PRIOR FILING DATE: 1998-10-21

PRIOR APPLICATION NUMBER: 60/105,234

PRIOR FILING DATE: 1998-01-28

PRIOR APPLICATION NUMBER: 00/105,234

PRIOR FILING DATE: 1998-01-28

PRIOR PRIOR FILING DATE: 1998-01-28

PRIOR FILING DATE: 1998-01-28

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PRIOR PRIOR PRIOR DATE: 1998-01-28
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; LOCATION: 534, 596, 615, 633, 641, 648, 656, 710, 729, 736, 744, 748,
; LOCATION: 749, 751, 752
; OTHER INFORMATION: n = A,T,C or G
US-10-779-543-22493
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GENERAL INFORMATION:
APPLICANT: Williams et al
TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II
FILE REFERENCE: 2300-21302
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                                                                                                              292 TCAGTAAAAACACTTTTAGAGATTGTGTTTCCTTTTTGTGAG 334
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                                                                                                                                                                                                                                                                                                                                                                  Sequence 22493, Application US/10779543
GENERAL INFORMATION:
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Best Local Similarity 24.3:
Matches 25; Conservative
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ORGANISM: Homo sapiens
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US-10-779-543-22493
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TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE IT
FILLE REFERENCE: 2300-21302
CURRENT APPLICATION NUMBER: US/10/779,543
CURRENT FILING DATE: 2004-02-12
PRIOR FILING DATE: 2002-02-12
PRIOR FILING DATE: 1994-12-21
PRIOR FILING DATE: 1997-12-23
PRIOR FILING DATE: 1997-12-23
PRIOR FILING DATE: 1997-12-23
PRIOR FILING DATE: 1998-10-21
PRIOR FILING DATE: 1998-10-21
PRIOR FILING DATE: 1998-10-21
PRIOR FILING DATE: 1998-10-21
PRIOR APPLICATION NUMBER: 60/080,664
PRIOR FILING DATE: 1998-10-21
PRIOR FILING DATE: 1998-10-21
PRIOR FILING DATE: 1998-10-21
PRIOR FILING DATE: 1998-10-21
PRIOR FILING DATE: 2000-04-10
PRIOR FILING DATE: 2000-04-10
PRIOR FILING DATE: 2000-04-10
PRIOR FILING DATE: 2000-04-10
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LOCATION: 2, 3, 4, 8, 19, 21, 37, 40, 44, 45, 54, 57, 65, 66, 71, 500,
LOCATION: 566, 574, 575, 576, 597, 604, 617, 633, 640, 656, 660, 680,
LOCATION: 684, 694, 709, 716, 720, 730, 734, 750, 755, 762, 763, 766
OTHER INFORMATION: n = A,T,C or G
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PRIOR PELING DATE: 2004-02-12
PRIOR PELING DATE: 2002-02-15
PRIOR PELING DATE: 2002-02-15
PRIOR PELING DATE: 10076,555
PRIOR PELING DATE: 1098-12-21
PRIOR PELING DATE: 1998-12-23
PRIOR PELING DATE: 1997-12-23
PRIOR PILING DATE: 1997-12-23
PRIOR PILING DATE: 1997-12-23
PRIOR PILING DATE: 1997-12-23
PRIOR PILING DATE: 1998-04-03
PRIOR PLING DATE: 1998-04-03
PRIOR PELING DATE: 1998-10-21
PRIOR PELING DATE: 1998-10-21
PRIOR PELING DATE: 1999-01-28
PRIOR PELING DATE: 1998-02-34
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 22418
LENGTH: 769
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APPLICANT: Williams et al

TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED

TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II

FILE REFERENCE: 2300-21302

CURRENT APPLICATION NUMBER: 10/076,555

PRIOR APPLICATION NUMBER: 10/076,555

PRIOR FILING DATE: 2002-02-15

PRIOR APPLICATION NUMBER: 09/217,471

PRIOR FILING DATE: 1998-12-21

PRIOR FILING DATE: 1998-12-21

PRIOR FILING DATE: 1998-10-21

PRIOR FILING DATE: 1998-04-03

PRIOR FILING DATE: 1998-01-28

PRIOR FILING DATE: 1999-01-28

PRIOR FILING DATE: 1999-01-28

PRIOR FILING DATE: 1999-01-28

PRIOR FILING DATE: 1998-01-28

PRIOR FILING DATE: 1998-01-28
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Remaining Prior Application data removed - See File Wrapper or FALM.
NUMBER OF SEQ ID NOS: 23767
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23307
LENGTH: 929
                                                                                                                                                                                                                                                                     - See File Wrapper or PALM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 5, 7, 9, 12, 15, 17, 19, 20, 27, 33, 46, 62, 63, 64, 6
LOCATION: 67, 74, 76, 509, 613, 645, 651, 655, 666, 678, 715, 71
LOCATION: 729, 742, 772, 776, 779, 780, 781, 783, 786, 787, 788
OTHER INFORMATION: n = A,T,C or G
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25.6%; Score 27.4; DB 6; Length 789;
Best Local Similarity 24.3%; Pred. No. 5.4;
Matches 25; Conservative 9; Mismatches 69; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 23767
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 23307, Application US/10779543 GENERAL INFORMATION:
PRIOR FILING DATE: 1999-01-28
PRIOR PEDELCATION NUMBER: 60/072,910
PRIOR FILING DATE: 1998-01-28
PRIOR APPLICATION NUMBER: 60/075,954
PRIOR APPLICATION NUMBER: 60/080,114
PRIOR FILING DATE: 1998-03-31
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S-10-779-543-22415
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APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOOUSSOS CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10805
LENGTH: 1790242
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                   916,
                   858, 869, 882, 912,
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APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
ITTLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C21
CURRENT APPLICATION NUMBER: US/10/775,972
CURRENT FILING DATE: 2004-02-10
NUMBER OF SEQ ID NOS: 563
SOFTWARE FEATSEQ for Windows Version 4.0
SEQ ID NO 126
LENGTH: 3552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.0%; Score 24.6; DB 6; Length 3552; 27.2%; Pred. No. 43; ive 8; Mismatches 51; Indels 0
                                                                                                                                   Length 929;
                                                                                                                                                                                 Indels
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                                                                                                                                                                                   . 69
                                                                                                                                   25.6%; Score 27.4; DB 6; 24.3%; Pred. No. 5.6; tive 9; Mismatches 69;
NAME/KEY: misc_feature
LOCATION: 649, 788, 791, 795, 806, 818,
LOCATION: 919, 920, 921, 923, 926, 927,
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                           Best Local Similarity 24.3
Matches 25; Conservative
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Matches 22, Conservative
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; ORGANISM: Homo sapiens
US-10-775-972-126
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or insertion/deletion polymorphism (see Tables 1-
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CURRENT APPLICATION NUMBER: US/10/673,523
CURRENT FILING DATE: 2003-01-15
PRIOR PAPLICATION NUMBER: US/10/012,984
PRIOR FILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 92
                                                                                                                                                                                                                                                                                                     Sequence 10627, Application US/10767471
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 184809
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                                            4 AAAUNNNNUNAUAUGUNNNNNNCUNNNUUUNNNNNAAAAANUANAAAACAUNNNNNCUUN
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Indels
                                                                                                                                           770 AGTATATTTTCTTAATTAAAGAGCTTAAAAATAAGTTTTGTA 812
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (1)...(184809)
; OTHER INFORMATION: n = A,T,C or G, US-10-767-471-10627
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12;
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OTHER INFORMATION: unknown
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US-10-767-471-10627/c
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NAME/KEY: unsure
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LOCATION: 14994
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US-10-673-523-14/c
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LENGTH: 104000
  20;
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    Matches
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TITLE OF INVENTION: Method and System for Identifying Biological Entities in
TITLE OF INVENTION: Biological and Environmental Samples
FILE REPERENCE: 36609-183264 (SAICO007-PCT)
CURRENT APPLICATION NUMBER: PCT/US04/02000
CURRENT FILING DATE: 2004-01-23
PRIOR PPLICATION NUMBER: US 60/441,745
PRIOR FILING DATE: 2003-01-23
PRIOR FILING DATE: 2003-01-23
PRIOR FILING DATE: 2003-01-23
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TITLE OF INVENTION: Method and System for Identifying Biological Entities in
TITLE OF INVENTION: Biological and Environmental Samples
FILE REFERENCE: 36609-183264 (SAICCO87-PCT)
CURRENT APPLICATION NUMBER: PCT/USO4/02000
CURRENT FILING DATE: 2004-01-23
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                                                                                                                       3 AAAAUMNINIUMAUAUGINININININCUNININUUUUMNINININAAAAANUANAAAACAUNINININCUU 62
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                        Length 1790242;
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                                                                                                                                                                                                                        69; Indels
                                                                             Indels
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19.0%; Pred. No. 36;
                                                                          72;
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Best Local Similarity 19.0%; Pred. No. 36;
Matches 19; Conservative 12; Mismatches
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Pred. No. 46;
                                                                               9; Mismatches
                                Score 24.6; |
Pred. No. 73;
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PRIOR FILING DATE: 2003-01-23
PRIOR PELING DATE: 2003-01-23
PRIOR FILING DATE: 2003-01-23
NUMBER OF SEQ ID NOS: 3242
                                                                                                                                                                                                                                                                                                                                                                    PCT-US04-02000-361/c; Sequence 361, Application PC/TUS0402000; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 172, Application PC/TUS0402000 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 3242
SOFTWARE: Patentin version 3.2
SEQ ID NO 361
LENGTH: 500
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SEQ ID NO 172
LENGTH: 1000
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19.4%;
                                23.0%;
                                                                               Conservative
                             Query Match
Best Local Similarity
Matches 24; Conserv
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Best Local Similarity
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; ORGANISM: Clos'
PCT-USO4-02000-172
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Gaps

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us-09-646-651c-2.rnpn

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PEATURE:

NAME/KEY:
UOCATION: 14997

OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: unsure
LOCATION: 14999

OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: unsure
LOCATION: 15000

OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: unsure
LOCATION: 15001

OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: unsure
LOCATION: 15003

OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: unsure
LOCATION: 15005

OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: unsure
LOCATION: 15005

OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: unsure
LOCATION: 15006

OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: unsure
LOCATION: 15006

OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: unsure
LOCATION: 15006

OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: unsure
LOCATION: 15009

OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: unsure
LOCATION: 15009

OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: unsure
LOCATION: 15000

OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: unsure
LOCATION: 15000

OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: unsure
LOCATION: 15000

OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: unsure
LOCATION: 15010

OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: unsure
LOCATION: 15010
OTHER INFORMATION: unknown FEATURE:
NAME/KEY: unsure
LOCATION: 14995
OTHER INFORMATION: unknown FEATURE:
NAME/KEY: unsure
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LOCATION: 15012
OTHER INFORMATION: unknown
                                                                                                                                                                           LOCATION: 14996
OTHER INFORMATION: unknown
FEATURE:
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PEATURE:

NAME/KEX: unsure
LOCATION: 15016
OTHER INFORMATION: unknown
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NAME/KEY: unsure
LOCATION: 15017
OTHER INFORMATION: unknown
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NAME/KEY: unsure
LOCATION: 15019
OTHER INFORMATION: unknown
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NAME/KEY: unsure
LOCATION: 15020
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LOCATION: 15026
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NAME/KEY: unsure
LOCATION: 15029
OTHER INFORMATION: unknown
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OTHER INFORMATION: unknown
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NAME/KEY: unsure
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CCCATION: 15013
OTHER INFORMATION: unknown
FEATURE:
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OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: unsure
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OTHER INFORMATION: unknown
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APPLICANT: Sahin, Ugur
APPLICANT: Turce;, Ozlem
APPLICANT: Turce;, Ozlem
APPLICANT: Turce;, Ozlem
APPLICANT: Turce;, Ozlem
APPLICANT: Ludewig, Burkhard
TITLE OF INVENTION: Method for identifying biologically active structures of microbia
TITLE OF INVENTION: pathogens
FILE REPERENCE: 03-757
CURRENT APPLICATION NUMBER: US/10/468,591A
CURRENT FILING DATE: 2004-02-26
FRIOR FILING DATE: 2002-02-22
FRIOR FILING DATE: 2001-02-22
FRIOR FILING DATE: 2001-02-22
NUMBER: OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Lyme Disease Vaccines
FILE REFERENCE: PE481US
CURRENT APPLICATION NUMBER: US/09/830,230A
CURRENT FILING DATE: 2001-09-27
PRIOR PELICATION NUMBER: PCT/US98/12718
PRIOR PELING DATE: 1998-06-18
PRIOR PILING DATE: 1997-09-03
PRIOR PILING DATE: 1997-07-22
PRIOR PLING DATE: 1997-07-22
PRIOR PLING DATE: 1997-07-22
PRIOR PLING DATE: 1997-07-22
PRIOR PILING DATE: 1997-06-20
NUMBER OF SEQ ID NOS: 756
SOFTWARE: PACENTIN Ver. 2.0
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Pred. No. 92
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             US-10-468-591A-8/c; Sequence 8, Application US/10468591A; GENERAL INFORMATION:
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21.2%;
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Best Local Similarity 21.4.
Thes 21; Conservative
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ORGANISM: Vaccinia virus
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ORGANISM: Homo sapiens
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1336 T 1336
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US-09-830-230A-324
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LENGTH: 3258
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
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Pred. No. 1.3e+02;
8; Mismatches 72;
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NUMBER OF SEQ ID NOS: 50231
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 10732
LENGTH: 138434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: CL001505
CURRENT APPLICATION NUMBER: US/10/767,471
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ilarity 23.1%;
Conservative 8
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LOCATION: 15035
OTHER INFORMATION: unknown
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LOCATION: 15031
OTHER INFORMATION: unknown
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Best Local Similarity 23.1
Matches 24; Conservative
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CORGANISM: Homo sapiens
US-10-767-471-10732
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Best Local Similarity
Matches 24; Conserv
                                        FEATURE:
NAME/KEY: unsure
LOCATION: 15032
OTHER INFORMATION: u
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LOCATION: 15036
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S-09-830-230A-323
Sequence 322, Application US/09830230A
GENERAL INFORMATION:
APPLICANT: Human Genome Science, Inc.
TITLE OF INVENTION: Lyme Disease Vaccines
FILE REFERENCE: P8481US
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US/09/830,230A
CURRENT FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 60/057,483
PRIOR FILING DATE: 1997-09-03
PRIOR FILING DATE: 1997-09-03
PRIOR FILING DATE: 1997-05-22
PRIOR PILING DATE: 1997-07-22
PRIOR APPLICATION NUMBER: 60/053,344
PRIOR FILING DATE: 1997-07-22
PRIOR PILING DATE: 1997-07-22
PRIOR APPLICATION NUMBER: 60/053,377
PRIOR FILING DATE: 1997-07-22
PRIOR PILING DATE: 1997-07-22
PRIOR APPLICATION NUMBER: 60/050,359
PRIOR PILING DATE: 1997-06-20
NUMBER OF SEQ ID NOS: 756
SOFTWARE: PATENTIN VEY: 2.0
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Query Match 21.9%; Score 23.4; DB 5; Length 3354; Best Local Similarity 21.2%; Pred. No. 93; Matches 21; Conservative 9; Mismatches 69; Indels 0; Gaps

TYPE: DNA ORGANISM: Homo sapiens S-09-830-230A-323

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45.7		43.8	43.8	43.8	43.5	41.1	41.1	41.1	41.1	41.1	41.1	41.1	38.8	38.8	38.8	38.8	38.8	38.3	38.2
213.5	206	204.5	204.5	204.5	203	192	192	192	192	192	192	192	181	8	8	181	181	179	178.5
7 7 9 1	1.7	28	29	30	31	32	33	34	35	36	37	38	<u>ო</u>	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1

Bioactive, metal, RNA polypeptide, RNP, modulation, analysis, angiogenesis, vascular state, mammalian tissue, transfer, cell, genetic information, selective, alteration, nucleic acid content, leukocyte, pig, monocyto-CuRNP. Component of bioactive metal RNA polypeptide. AAW01826 standard; protein; 91 AA. (first entry) 16-OCT-1997 Sus scrofa. AAW01826; AAW01826

96DE-01028895. DE19628895-A1. 17-JUL-1996; 23-JAN-1997. 

(FRAU ) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.

95DE-01025992. 95DE-01030500.

17-JUL-1995; 18-AUG-1995;

Kiesewetter S, Heilmeyer LMG; ы, Wissler JH, Logemann

WPI; 1997-088586/09. N-PSDB; AAT62569.

Bioactive metal RNA polypeptide - useful for modulating angiogenesis, etc.

Claim 1; Page 15; 16pp; German.

A novel bioactive metal RNA polypeptide (RNP) has a RNA component including the sequence AAT62568 and a polypeptide component having the sequence AAM01826, which is encoded by AAT62569. The RNP, or anti-RNP immunoglobulins, can be used to modulate and/or analyse angiogenesis and the vascular state of mammalian tissue, transfer genetic information in cells and selectively alter the nucleic acid content of cells. Leukocytes from pig's blood were cultured in medium, and the supernatant treated with NH4 sulphate at 13, 45 and 90% saturation to precipitate protein fractions. The residual supernatant was diltued to 45% NH4 sulphate saturation and concentrated by ultrafiltration using a 0.5 kD membrane.

give 8 mg of product described as monocyto-

The retenate was purified to

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This invention describes novel copper-containing ribonucleoproteins which are ternary complexes of an $100 protein, copper ions, and RNA comprising the following consensus sequence or its complement GGAAAANNNUNNUNAGUAIL CUNNUUNNUUNNUNNUNAAAAAOLUND-SCUUNAGNO-13AGAA-AUNO-16UUAGCAG where CCUNNUUUNNNUNNAAAAAO-1UANAAAACANNO-5CUUNAGNO-13AGAA-AUNO-16UUAGCAG where N = G, A, U or C. The ribonucleoproteins are stated to have the following properties (1) cell-selective morphogenic action in vitro on isolated primary and/or cloned blood capillary endothelial cells in culture for the non-mitogenic induction of the change in cell phenotype from the confluent state, for non-mitogenic alteration of the spatiotemporal supracellular organisation of cells into three-dimensional organoid, capillary-like structures in culture, (2) a specific chemctropic action on blood vessels in vivo, (3) induction of directional growth of blood vessels in vivo and (4) induction of neovascularisation of tissues through directed ingrowth of blood vessels. Their use for modulating angiogenesis is claimed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW93819 standard; peptide; 91
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                                                                                     Query Match
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Conservative
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                                                                 Sequence 91
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CURNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents the CAAF1 calcium-binding protein isolated from bovine amnictic fluid. CAAF1 belongs to the S100 protein family, which includes calcyclin, MRP8, and MRP14. Intracellular calcium ion concentration is one of the key factors for intracellular signal transduction. The calcium signals are transduced by various calcium-binding proteins, such as the protein encoded by this sequence. CAAF1 is normally expressed in squamous epithelial cells, neutrophils and macrophages, but atypical epithelial cells are negative for CAAF1 and overexpression is observed in several types of cancer cells and neutrophils/macrophages infiltrating cancercous lesions. Detection of CAAF1 (using antibodies in usual immunoassays) can be used to diagnose (or monitor) inflammation, neoplasia (particularly, squamous cell).
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                                                                                                                                                                                                                                                                                                                                                                                               Calcium binding protein; bovine; amniotic fluid; S100 protein family; intracellular signal transduction; squamous epithablal cell; neutrophil; macrophage; cancer; cancerous lesion; inflammation; neoplasia; cervix; squamous cell carcinoma; skin; oesophagus; CAAFI; lung; blood disease.
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                                                                                                  1 TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTKDQGTIDKIFQNL
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                                   Indels
100.0%; Score 467; DB 2;
100.0%; Pred. No. 7.5e-46;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                             AAW03563 standard; protein; 92
                                                                                                                                                                                                                                                                                                                                                              Calcium binding protein CAAF1.
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95JP-00070468.
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06-MAR-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes an isolated human EN-RAGE (extracellular novel receptor for advanced glycation end products) peptide (PI). The EN-RAGE peptide binds to RAGE which is a member of the immunoglobulin superfamily of cell-surface molecules. A compound capable of inhibiting the interaction of EN-RAGE with RAGE is useful for the suppression of inflammation resulting from systemic lupus erythematosus, inflammatory lings nephritis, septic abook, endotoxaemia, or an autoimmune or inflammatory disorder in which the recruitment of EN-RAGE containing inflammatory cells occurs. The compound is also useful for the treatment of systemic lupus erythematosus, inflammatory lupus nephritis in a subject. The human EN-RAGE peptide is useful for identifying compounds the bovine CAAFL which shows homology to the human EN-RAGE N-terminal amino acid sequence
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                                                                                          DANQDEQVSFKEFVVLVTDVLITAHDNIHKE
                                                                                                                                                    62 DADKDGAVSFEEFVVLVSRVLKTAHIDIHKE
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Best Local Similarity
Matches 73; Conserv
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receptor for advanced glycation endproduct; inflammation; inhibition; antiinflammatory; immunoglobulin; cell surface molecule; septic shock; systemic lupus erythematosus; inflammatory lupus nephritis; endotoxaemia; autoimmune disorder; inflammatory disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human EN-RAGE (extracellular novel receptor for advanced glycation end products) peptide, useful for identifying anti-inflammatory compounds that inhibit its interaction with RAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    novel receptor for advanced glycation and products) peptide (PI). The EN-RAGE peptide binds to RAGE which is a member of the immunoglobulin superfamily of cell-surface molecules. A compound capable of inhibiting the interaction of EN-RAGE with RAGE is useful for the suppression of inflammation resulting from systemic lupus erythematosus, inflammatory lupus nephritis, septic shock, endotoxaemia, or an autoimmune or inflammatory cells occurs. The compound is also useful for the treatment of systemic lupus erythematosus, inflammatory lupus nephritis in a subject. The human EN-RAGE peptide is useful for identifying compounds that inhibit its interaction which RAGE. The present sequence represents the bovine corneal antigen which shows homology to the human EN-RAGE per security.
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81.1%; Pred. No. 3e-34;
ive 9; Mismatches
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DADKDGAVSFEEFVVLVSRVLKTAHIDIHK
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                                                                                                 AAY90764 standard; protein; 90
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Best Local 3, Conservative
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standard; protein; 92

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The present sequence represents a human protein, which is used in the method of the invention. The specification describes a method which uses at least one polypeptide or polymucleotide sequence belonging to the perlecan, precursor of the terinol-binding plasma protein, precursor of the ganglioside GMZ activator, calgranulin B or saposin B protein families. The method is used for detecting, preventing or treating a degenerative, neurological and/or auto-immune disease. The polymucleotides and polypeptides are used for diagnosis, prognosis, prevention and treatment of multiple sclerosis (in its various forms and phases). They may also be useful in cases of e.g. Alzheimer's and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene therapy (expression of sense or antisense sequences). They can also be used to assess efficacy of potential therapeutic agents, particularly compounds that reduce or inhibit toxicity towards glial cells
                                                                                                                                                                                                                                                                                                                       Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine; ganglioside GM2 activator; saposin B; degenerative disease; glial cell; neurological disease; auto-immune disease; multiple sclerosis; toxicity; Alzheiner's disease; Parkinson's disease; reactive phic lateral sclerosis; rheumatoid polyarthritis; lupus erythematosus; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTKDQGTIDKIFQNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting, preventing and treating degenerative, neurological and autoimmune diseases, particularly multiple sclerosis, using specified polypeptides or related nucleic acid or ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Santoro L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.1%; Score 332; DB 4; 70.3%; Pred. No. 2.5e-30; tive 10; Mismatches 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Malcus C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91
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                                                                                                                                                                                                                                                         Amino acid sequence of a human protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Charles M,
                               AAB31909 standard; protein; 91 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 167; 209pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JUL-2000; 2000WO-FR002057.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99FR-00009372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (INMR ) BIOMERIEUX STELHYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 70.3%
Matches 64; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-159475/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 91 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200105422-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roecklin D,
                                                                                                                                                                               15-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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AAB31909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human ammiotic fluid. CARTI belongs to the S100 protein family, which includes calcyclin, MRP8, and MRP14. Intracellular calcium ion concentration is one of the key factors for intracellular signal transduction. The calcium signals are transduced by various calciumbinding proteins, such as this protein. CAAFI is normally expressed in squamous epithelial cells, neutrophils and macrophages, but arypical epithelial cells are negative for CAAFI and overexpression is observed in several types of cancer cells and neutrophils/macrophages, infiltrating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human or bovine calcium binding protein and related nucleic acid - is a marker for inflammation, neoplasia, skin and blood diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                           Calcium binding protein; human; amniotic fluid; S100 protein family; intracellular signal transduction; squamous epithelial cell; neutrophil; macrophage; cancer; cancerous lesion; inflammation; neoplasia; cervix; squamous cell carcinoma; skin; oesophagus; CAAFI; lung; blood disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancerous lesions. Detection of CAAFI (using antibodies in usual immunoassays) can be used to diagnose (or monitor) inflammation, neoplasia (particularly squamous cell carcinoma of the skin, oesophagus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TKLEEHLEGIVNIFHQYSVRKGHFDTLSKGELKQLLTKELANTIKNIKDKAVIDEIFQGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents the CAAF1 calcium-binding protein isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.1%; Score 332; DB 2; Length 92; 70.3%; Pred. No. 2.5e-30; ive 10; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ung and cervix), and skin and blood diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kimura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamamura
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW24137 standard; protein; 92
                                                                                              Calcium binding protein CAAF1.
                                                                                                                                                                                                                                                                                                               95EP-00119045
                                                                                                                                                                                                                                                                                                                                               95JP-00045564
                                                                                                                                                                                                                                                                                                                                                                95JP-00070468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hitomi J, Yamaguchi
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                                                                                                                                                                                                                                                                                                                                                                                                (TOFU ) TONEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                               (HITO/) HITOMI J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAT39346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 92 AA;
                                                                                                                                                                                                                                                                                                                04-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                06-MAR-1995;
                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                 06-MAR-1995;
                                                              01-MAY-1997
                                                                                                                                                                                                                                              EP731166-A2
                                                                                                                                                                                                                                                                                11-SEP-1996
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Matches
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(first entry)

28-JAN-1998

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This is a human chemotactic cytckine I polypeptide. The encoding polymucleotide, along with a vector and a host cell can be used for the recombinant production of the chemotactic cytokine. Cytckine agonists and antagonists can be used for the treatment of a patient requiring a chemotactic cytokine I and for the treatment of a patient requiring the inhibition of a chemotactic cytokine I polypeptide, respectively. The chemotactic cytokine is used to treat tumours, chronic infection, leukaemia and T-cell mediated autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      calculum-binding protein; calcium homeostasis; cardiac muscle; pumping capacity; myocardial cell; systolic calcium ion release; sarcoplasmic reticulum; cardiac disease; hypertension; rhythm disorder;
                                                         chemotactic cytokine; tumour; autoimmune disease; antagonist; agonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S100 protein; human; treatment; cardiomyopathy; cardiac insufficiency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTKDQGTIDKIFQNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 TKLBEHLEGIVNIFHQYSVRKGHFDTLSKGELKQLLIKELANTIKNIKDKAVIDEIFQGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DANQDEGVSFKEFVVLVTDVLITAHDNIHKE 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 DANQDEQVDFQEFISLVAIALKAAHYHTHKE 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 12; Page 48-49; 64pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding chemotactic cytokine chronic infection, leukaemia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB45542 standard; protein; 92
Human chemotactic cytokine I.
                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 70.34
Matches 64; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-351075/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAT85774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 92 AA;
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                                                                                                                                                                                 WO9723640-A1
                                                                                                                                                                                                                                                                                                                                                                            26-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yu G,
                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                  26-DEC-1995;
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This invention describes a novel composition for treating primary or secondary cardiomyopathy or cardiac insufficiency contains at least one Sloo protein (I) or mucleic acid (II) encoding (I), or their mutents or fragments, or a gene transfer vector containing (II), optionally commulated with auxiliaries and/or carriers. (I) are calcium-binding protein involved in calcium homeostasis, so their overexpression in cardiac muscle will improve pumping capacity (and overall capacity) of the heart. In cultured myocardial cells they increase the contraction and cardiac muscle will improve pumping capacity (and overall capacity) of the heart. In cultured myocardial cells they increase the contraction and cardiac muscle will improve pumping capacity (and overall capacity) of the heart. In cultured myocardial cells they increase the contraction and capacity (and overall calcium ion release from the sarcoplasmic reticulum (SM) and calcium re-uptake by SR. (I) are used to treat cardiomyopathy (CMP) where inherited or caused by contaction and istension and structural disease caused by rhythm disorders or valve defects, generally any condition associated with reduced contractile force. Unlike calmodulin, which is expressed the underlying defect in the sarcoplasmic reticulum (SR) that causes cardiac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine; ganglioside GMZ activator; saposin B; degenerative disease; glial cell; neurological disease; auto-immune disease; multiple solerosis; toxicity; Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis; rheumatoid polyarthritis; lupus erythematosus; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTKDQGTIDKIPQNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TKLBEHLEGIVNI FHQYSVRKGHFDTLSKGELKQLLTKELANTIKNIKDKAVIDBIFQGL
                                                                                                                                                                                                                                      Composition containing $100 protein, corresponding nucleic acid or vector, useful for treating cardiomyopathy and cardiac insufficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      th 71.1%; Score 332; DB 3; L Similarity 70.3%; Pred. No. 2.5e-30; 64; Conservative 10; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of a human protein.
                                                                                                                                                                                                                                                                                                 Claim 35; Page 20; 36pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB31911 standard; protein; 92
99DE-01015485
                                      99DE-01015485
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                                                                                                                                        Remppis A;
                                                                                                                                                                           WPI; 2000-673510/66.
                                                                                                                                                                                                 N-PSDB; AAC81812
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07-APR-1999;
                                    07-APR-1999;
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                                                                                                                                  Katus HA,
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Best Local S
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                                                                           (KATU/)
                                                                                               (REMP/)
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Length 92;

71.1%; Score 332; DB 2; Length 92 70.3%; Pred. No. 2.5e-30; ive 10; Mismatches 17; Indels

(first entry)

to treat, e.g. tumours,

chemotactic cytokine I - used

Su JY;

Gentz R,

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Alfonso

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method of the invention. The specification describes a method which uses at least one polypeptide or polymucleotide sequence belonging to the perlecan, precursor of the retinol-binding plasma protein, precursor of the ganglioside GMZ activator, calgranulin B or aposin B protein degenerative, neurological and/or ato-binding, preventing or treating a degenerative, neurological and/or ato-binding plasma. The polymocleotides and polypoppides are used for diagnosis, prognosis, prevention and treatment of multiple sclerosis (in its various forms and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           be used to assess efficacy of potential therapeutic agents, particularly compounds that reduce or inhibit toxicity towards glial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phases). They may also be useful in cases of e.g. Alzheimer's and Parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid polyarthritis and lupus erythematosus, including use as vaccines and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detecting, preventing and treating degenerative, neurological and autoimmune diseases, particularly multiple sclerosis, using specified polypeptides or related nucleic acid or ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence represents a human protein, which is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene therapy (expression of sense or antisense sequences). They be used to assessed as the contract of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 168; 209pp; French.
17-JUL-2000; 2000WO-FR002057
                                                                                                                                                                                                                            99FR-00009372
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INMR ) BIOMERIEUX STELHYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kolbe H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-159475/16.
                                                                                                                                                                                                                            15-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roecklin D,
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Sequence 92 AA;

Query Match

1 TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTKDQGTIDKIFQNL Gaps .; 0 71.1%; Score 332; DB 4; Length 92; 70.3%; Pred. No. 2.5e-30; ive 10; Mismatches 17; Indels 61 DANQDEQVSFKEFVVLVTDVLITAHDNIHKE 91 64; Conservative Local Similarity Best Loca Matches à ò

DANQDEQVDFQEFISLVAIALKAAHYHTHKE 92

AAB31907 standard; protein; RESULT 11 **AAB**3190'

AAB31907;

ΑĀ

92

Amino acid sequence of a human protein. (first 15-MAY-2001

Human, perlecan, retinol-binding plasma protein, calgranulin B; vaccine, ganglioside GM2 activator, saposin B; degenerative disease, glial cell, neurological disease; auto-immune disease; multiple sclerosis, toxicity; Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis; rheumatoid polyarthritis; lupus erythematosus; gene therapy.

Homo sapiens.

WO200105422-A2

25-JAN-2001

17-JUL-2000; 2000WO-FR002057

99FR-00009372 15-JUL-1999;

(INMR ) BIOMERIEUX STELHYS

Perron H; Santoro L, Malcus C, Charles M, Kolbe H, WPI; 2001-159475/16. Roecklin D, 

autoimmune diseases, particularly multiple sclerosis, using specified polypeptides or related nucleic acid or ligand. neurological and Detecting, preventing and treating degenerative,

Perron

Santoro L,

Malcus C,

Charles M,

Claim 1; Page 166-167; 209pp; French.

The present sequence represents a human protein, which is used in the method of the invention. The specification describes a method which uses at least one polypeptide or polynuclectide sequence belonging to the perfectan, precursor of the retinol-binding plasma protein, precursor of the ganglioside GM2 activator, calgranulin B or saposin B protein the ganglioside GM2 activator, calgranulin B or saposin B protein canning an each of is used for detecting, preventing or treating a degenerative, neurological and/or auto-immune disease. The polynucleotides and polypeptides are used for diagnosis, prognosis, provention and treatment of multiple sclerosis (in its various forms and passes). They may also be useful in cases of e.g. Alzheimer's and Parkinson's diseases, amyotrophic lateral sclerosis, theumatoid polyarchritis and lupus erythematosus, including use as vaccines and in gene therapy (expression of sense or antisense sequences). They can also be used to assess efficacy of potential therapeutic agents, particularly compounds that reduce or inhibit toxicity towards glial cells

Sequence 92 AA;

also

Can

0; Length 92; Indels 71.1%; Score 332; DB 4; 70.3%; Pred. No. 2.5e-30; ive 10; Mismatches 17; Conservative Similarity 64; Query Match Best Local Matches

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1 TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTKDQGTIDKIFQNL

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61

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16 92 DANODEOVSFKEFVVLVTDVLITAHDNIHKE DANQDEQVDFQEFISLVAIALKAAHYHTKE 61 à

AAB31908

AAB31908 standard; protein; 92 AA.

(first entry) 15-MAY-2001

Amino acid sequence of a human protein.

Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine; ganglioside GM2 activator, saposin B, degenerative disease, glial cell, neurological disease, auto-immune disease, multiple sclerosis, toxicity, Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, rheumatoid polyarthritis; lupus erythematosus; gene therapy

sapiens Homo WO200105422-A2.

17-JUL-2000; 2000WO-FR002057.

99FR-00009372 .5-JUL-1999; 

(INMR ) BIOMERIEUX STELHYS.

Perron H; ŭ Santoro ΰ Malcus Σ Charles Kolbe H, Roecklin D,

WPI; 2001-159475/16. FFK@Xbbbbbbbbbbbb

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Detecting, preventing and treating degenerative, neurological and autoimmune diseases, particularly multiple sclerosis, using specified polypeptides or related nucleic acid or ligand.
                                                                                                                                                                                           Claim 1; Page 167; 209pp; French
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method of the invention. The specification describes a method which uses at least one polypeptide or polymucleotide sequence belonging to the series of the retinol-binding plasma protein, precursor of the retinol-binding plasma protein, precursor of the ganglioside GMZ activator, calgranulin B or saposin B protein families. The method is used for detecting, preventing or treating a clegenerative, neurological and/or auto-immune disease. The polymucleotides and polypeptides are used for diagnosis, prognosis, prevention and treatment of multiple sclerosis (in its various forms and phases). They may also be useful in cases of e.g. Alzheimer's and parkinson's diseases, amyotrophic lateral sclerosis, rheumatoid polyarthritis and lupus erythematosus, including use as vaccines and in gene therapy (expression of sense or antisense sequences). They can also be used to assess efficacy of potential therapeutic agents, particularly compounds that reduce or inhibit toxicity towards glial cells present sequence represents a human protein, which is used in the

Sequence 92 AA;

TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTKDQGTIDKIFQNL Length 92; 17; Indels 71.1%; Score 332; DB 4; 70.3%; Pred. No. 2.5e-30; ive 10; Mismatches 17; 64; Conservative Best Local Similarity Query Match Matches

·;

93 61 DANQDEQVSFKEFVVLVTDVLITAHDNIHKE ~

62 DANQDEQVDFQEFISLVAIALKAAHYHTHKE 92

ADA93649;

ADA93649 standard; protein; 92 AA.

ESULT 13 DA93649

(first entry) 20-NOV-2003 Human calgranulin C protein SEQ ID NO:2.

inflammatory disease, calgranulin C; antiinflammatory; gene therapy; vasculitis; Kawaski disease; cystic fibrosis; chronic inflammatory disease; ulcerative colitis; Crohn's disease; chronic bronchitis; inflammatory arthritis; psoriatic arthritis; rheumatoid arthritis; seronegative arthritis; systemic onset juvenile rheumatoid arthritis; schougative arthritis;

acute inflammation; human

Homo sapiens.

WO2003069341-A2.

21-AUG-2003

17-FEB-2003; 2003WO-EP001575.

15-FEB-2002; 2002US-00077600.

(SWIT-) SWITCH BIOTECH AG. (SORG/) SORG C. (ROTH/) ROTH J.

Roth J; Sorg C,

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The present invention describes a method for diagnosing inflammatory diseases, which comprises determining the amount and/or concentration of calgarantin C polypeptide and/or nucleic acids encoding the polypeptide present in the biological sample. Also described are methods for treating or preventing an inflammatory disease in a mammal, and medical treatment of the mammal, where the treatment is based on the stage of the disease to be treated or prevented. Calgranulin C has antiinflammatory activity and can be used in gene therapy. The method is useful for diagnosing, treating or preventing inflammatory diseases, e.g. vasculitis (particularly kawasaki disease), cystic fibrosis, chronic inflammatory diseases like ulcerative collitis or Crohn's disease, chronic bronchitis, inflammatory arthritis (e.g. psoriatic arthritis, rheumatoid arthritis or seronegative arthritis), systemic onset juvenile rheumatoid arthritis or seronegative arthritis), systemic onset juvenile rheumatoid arthritis or seronegative arthritis), alsease, acute inflammation on the background of a inflammatory disease, or an exacerbation of an already present disease.

The method is also useful for diagnosing specific stages of inflammatory diseases, for determining the risk of relapse, and for discriminating between diseases with similar symptoms. The present sequence represents human calgranulin C, which is used in the exemplification of the present
                                                                                                              Diagnosing, treating or preventing inflammatory diseases comprises determining the amount and/or concentration of CALGRANULIN C polypeptide and/or nucleic acids encoding the polypeptide present in a biological
                                                                                                                                                                                                                                                       Claim 7; Page 64; 64pp; English.
                          WPI; 2003-671681/63.
N-PSDB; ADA93648.
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Sequence 92 AA;

61 2 TKLBEHLEGIVNIFHQXSVRKGHFDTLSKGELKQLLTKELANTIKNIKDKAVIDEIFQGL 1 TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTKDQGTIDKIFQNL Length 92; 17; Indels 71.1%; Score 332; DB 7; 70.3%; Pred. No. 2.5e-30; iive 10; Mismatches 17 61 DANODEQVSFKEFVVLVTDVLITAHDNIHKE 91 Local Similarity 70.3 Query Match Matches

ABG27582

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Ą. ABG27582 standard; protein; 95

(first entry) 18-FEB-2002

Novel human diagnostic protein #27573.

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.

Homo sapiens.

WO200175067-A2.

11-OCT-2001.

30-MAR-2001; 2001WO-US008631.

2000US-00540217. 2000US-00649167. 31-MAR-2000; 23-AUG-2000;

(HYSE-) HYSEQ INC

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Tang YT;
Liu C,
   WPI; 2001-639362/73
     N-PSDB; AAS91769
Drmanac RT,
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useful in of mutations New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity.

Claim 20; SEQ ID NO 57941; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in game therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging involving expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this spatent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 95 AA;

.; 0 65.5%; Score 306; DB 4; Length 95; 67.0%; Pred. No. 2.5e-27; ive 10; Mismatches 20; Indels 20; Indels Best\_Local Similarity 67.0 Matches 61; Conservative Query Match Best Local S

1 TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTKDQGTIDKIFQNL 60 

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à

61 DANODEQVSFKEFVVLVTDVLITAHDNIHKE 91

DANQDEQVDFQEFISLVAIALKAAHYHTHKE 95

AAW17062 standard; protein; 114 AA AAW17062

RESULT 15

AAW17062;

(first entry) 16-JUL-1997

Human multidrug resistance protein 14 (MRP14).

animal model; cell death inhibition; apoptosis; cell proliferation; HIV; human immunodeficiency virus; cancer; cystic fibrosis; neoplasia; tumour. Genetic engineering; MRP; multidrug resistance protein; transgenic;

Homo sapiens

25-MAR-1997

US5614397-A.

94US-00200016. 22-FEB-1994;

94US-00200016 22-FEB-1994;

(STRD ) UNIV LELAND STANFORD JUNIOR.

Lagasse E; Weissman I,

WPI; 1997-224943/20.

N-PSDB; AAT68322

Increasing life-span of mammalian haemato-lymphoid cells by transforming stem cells - with construct contg. cell-specific transcription initiator and gene encoding protein that increases lifetime, useful for drug screening and treatment.

Example 1; Col 33-34; 34pp; English.

Gene, the horpes virus thymidine kinase gene or an oncogene. Haematclymphoid cells are especially neutrophils and the construct doubles the lifespan of transgenic cells. Transgenic cells or transgenic animals produced are used for screening for substances and treatments that prevent or promote cell death. They can also be returned to the patient to modulate apoptosis, i.e. in the treatment of disorders related to abnormal cell proliferation or death. Typical applications are treatment of viral diseases, including HIV; cancer and cystic fibrosis AAW17062 is the human MRP14 protein. The transcriptional initiator of the MRP8 gene was used in a construct for expressing an open reading frame that increase the lifespan of a mammalian haematolymphoid cell, e.g. the mammalian bcl-2 gene, a CFTR (cystic fibrosis transmembrane regulator)

Sequence 114 AA;  45.7%; Score 213.5; DB 2; Length 114; 45.1%; Pred. No. 1.3e-16; tive 25; Mismatches 24; Indels 1; Conservative Local Similarity es 41; Conserv Query Match

1 TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTL-KNTKDQGTIDKIFQN 59 SQLERNIETIINTFHQYSVKLGHPDTLNQGBFKELVRKDLQNFLKKENKNEKVIEHIMED 65 g

LDANQDEQVSFKEFVVLVTDVLITAHDNIHK 90 09 ò

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64

5, 2004, 09:46:44 completed: March Search

Job time : 56 secs

SUMMARIES  1D  US-08-794-000-2 US-08-794-000-2 US-08-794-000-2 US-09-263-312-3 US-09-263-312-3 US-09-268-310D-20 US-09-270-455-20 US-09-268-310D-20 US-09-268-310D-2 US-09-263-312-4 US-09-205-680A-7	US-08-568-31 US-09-263-31 US-09-263-31 US-09-826-31 US-09-826-56 US-08-868-31 US-08-868-31 US-09-214-27 US-09-214-27 US-09-214-27 US-09-214-27 US-09-214-27 US-09-214-27 US-09-263-31 US-09-263-31 US-09-868-31 US-09-868-31
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1 TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTKOQGTIDKIFQNL 60

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	3 1	121	32.3	166	r	US-07	-987	-272A-7	Sequence	7, Appli
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	33	151	2	93		US-08	-385-	-241-1		1, Appli
	34	151	2	93		US-09	-214	-272-2		
	35	150	N	105		US-08	-918-	-727-6	Sednence (	6, Appli
	36	150	2	105		US-09	-202-	-680A-6	Sequence 6	i, Appli
	37	148	Н	97		US-07	-662	-198B-2	Sequence 2	2, Appli
	38	140.5	0	98		0S-08	-918-	-727-3	Sequence 3	i, Appli
	39	140.5	0	98		US-09	-202-	-680A-3	Sequence 3	i, Appli
	40	140.5	0	98		0S-09	-048-	-889-11	Sequence 1	1, Appl
	41	140	0	92		US-09	-621-	1-976-7537	Sequence 7	537, Ap
	42	137	σ	76		US-07-	-684	-272A-17		7, Appl
	43	136	σ	88	4	US-09	62.	$\alpha$ 1		7524, Ap
	44	136	σ	88	4	US-09	-621	-976-7526		,526, Ap
	45	136	6	89	1	US-07	-987	-272A-10	Sequence 1	o, Appl
						AL	ALIGNMENTS	ENTS		
RES	RESULT 1									
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	GENER	GENERAL INFORMATION	MATION:							
٠.	APP.	APPLICANT:								
•-	TIL	TITLE OF INVENTION:	VENTION		a]-(	Metal-Containing	ning	Ribonucleotide	ide Polypeptides	
•~	WON.	BER OF	SEQUENCE	4						
٠.	SO	COMPUTER READABLE	SADABLE	FORM:						
٠.	Σ	MEDIUM TYPE: Floppy disk	PE: FI	oppy o	i ak					
•-	ت ا	OMPUTER:	IBM P	C COMP	atik	ore.				
٠.	o i	OPERATING SYSTEM:	SYSTEM	- PG	Sog.	PC-DOS/MS-DOS				
•-	Ñ	SOFTWARE:	Paten	Patentin Release #1.0,	leas	se #1.		Version #1.30	(EPO)	
•-	CUR	CURRENT APPLICATION DATA	LICATIO	N DATE	٠.					
	A	APPLICATION NUMBER:	ON NUMB		13/0E	US/08/794,	000			
•-	Ēz.	FILING DATE:	TE:							
	PRI	PRIOR APPLICATION DATA:	CATION	DATA:						
•-	ď	APPLICATION NUMBER: PCT/DE96/0133	ON NUMB	ER: E	CT/I	)E96/0	1337			
	ניי ניין	ILING DA	TE: 17	-707-	966					
•-	P.K.L	FRIOR APPLICATION DATA:	CALTON	DATA:	•	L	6	,		
•-	ď Ė	AFFLICATION NOMBER: DE	ON NOME	EK:	<b>⊣</b> ι	ת ת ת	y y y	0		
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78.4%;
81.1%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
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Best Local Similarity
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LENGTH: 90
TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-270-455-19
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APPLICANT: YAMAGUCHI, JIRO
APPLICANT: YAMAGUCHI, KEN
APPLICANT: YAMAGURA, TATSUJI
TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEN: WYATT, GERBER, MELLER & O'ROURKE
STREET: 64b FLOOR
CITY
STREET: 64b FLOOR
CITY
STREET: NEW YORK CITY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 7-70468 and 7-45564 (both Japan)
FILING DATE: 3/6/95 and 3/6/95, respectively
ATTORNEY/AGENT INFORMATION:
NAME: KLEIN, MILTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19, Application US/09270455
Patent No. 613267
GENERAL INFORMATION:
APPLICANT: HITOMI, JIRO
APPLICANT: YAMAGUCHI, KEN
APPLICANT: KIMURA, TOKUJIRO
APPLICANT: KIMURA, TATSUJI
TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DANQDEQVSFKEFVVLVTDVLITAHDNIHKE 91
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                                                                                                                                                                                                                                                                                                                 ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE,3.50 INCH,720 Kb
MEDIUM TYPE: STORAGE
TYPE: STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM-PC COMPATIBLE
OPERATING SYSTEM: PC-DOS 6.2
SOFTWARE: WORDPERFECT 6.1
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/568,310D
FILING DATE: DECEMBER 6, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RELEVANT RESIDUES IN SEQ ID NO: RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 27101
REFERENCE/DOCKET NUMBER: 3316
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (212)953-3350
TELEFAX: (212)953-3352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS: LENGTH: 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: CDNA
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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US-09-270-455-19
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US-09-263-312-3

Sequence 3, Application US/09263312

Sequence 3, Application US/09263312

Sequence 3, Application US/09263312

Sequence 3, Application US/09263312

GENERAL INFORMATION:

APPLICANT: Schmidt, Ann Marie

APPLICANT: Stern, David

TITLE OF INVENTION: Extracellular No. 6555340el RAGE Binding Protein (EN-RAGE) and TITLE OF INVENTION: USES Thereof

FILE REFERENCE: 0575/55873-A

CURRENT APPLICATION NUMBER: US/09/263,312

CURRENT FILING DATE: 1999-03-05

NUMBER OF SEQ ID NOS: 5

SOSTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 19: FROM 1 TO 92
ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE STREET: 99 PARK AVENUE STREET: 6th FLOOR CITY: NEW YORK CITY STATE: NEW YORK
                                                                                                                                               COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH, 720 Kb
MEDIUM TYPE: STORAGE
COMPUTER: ISM-PC COMPATIBLE
OPERATING SYSTEM: PC-DOS 6.2
SOFTWARE: WORDPERFECT 6.1
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                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,455
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/568,310
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KLEIN, MILTON
REGISTRATION NUMBER: 27101
REFERENCE/DOCKET NUMBER: 3316
TELECOMMUNICATION INFORMATION:
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                                                                                                                                GENERAL INFORMATION:
APPLICANT: HITOMI, JIRO
APPLICANT: YAMAGUCHI, KEN
APPLICANT: NOVEL
TITLE OF INVENTION: NOVEL
CORESSPONDENCE ADDRESS:
ADDRESSPEN: WYATT, GERBER, MELLER & O'ROURKE
STREET: 6th FLOOR
STREET: 6th FLOOR
STREET: 6th FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: DECEMBER 6, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 7-70468 and 7-45564 (both Japan)
FILING DATE: 3/6/95 and 3/6/95, respectively
ATTORNEY/AGENT INFORMATION:
NAME: KLEIN, MILTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.1%; Score 332; DB 2; 70.3%; Pred. No. 8.7e-33; iive 10; Mismatches 17,
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FROM 1 TO 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: DISKETTE, 3.50 INCH,720 Kb MEDIUM TYPE: STORAGE COMPUTER: IBM-PC COMPATIBLE OPERATING SYSTEM: PC-DOS 6.2 SOTWARE: WORDBERFECT 6.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/568,310D FILING DATE: DECEMBER 6, 1995
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                                                                                                  Sequence 20, Application US/08568310D Patent No. 5976832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 20, Application US/09270455
; Patent No. 6313267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 33
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)953-3350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: HITOMI, JIRO
APPLICANT: YAMAGUCHI, KEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212)953-3352
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                      STREET: 6th FLOOR
CITY: NEW YORK CITY
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: KLEIN, MILTON
REGISTRATION NUMBER:
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Best Local Similarity
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ZIP: 100
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US-09-270-455-20
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Patent No. 6670136

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Schmidt, Ann Marie

APPLICANT: Schmidt, David

TITLE OF INVENTION:

TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE

TITLE OF INVENTION: US/09/826,589

CURRENT APPLICATION NUMBER: 105/09/826,589

CURRENT FILING DATE: 2001-04-05

SOFTWARE: PatentIn version 3.1

LENGTH: 90
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APPLICANT: Schwidt, Ann Marie

APPLICANT: Schwidt, David

APPLICANT: Schwidt, David

APPLICANT: Schwidt, David

TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE FILE REFERENCE: 0575/55873-B-PCT-US

CURRENT APPLICATION NUMBER: US/09/826,589

CURRENT FILING DATE: 2001-04-05

NUMBER OF SEQ ID NOS: 6

SEQ ID NO 4

SEQ ID NO 4

LENGTH: 90
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       Gaps
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6.7e-37;
ches 8; Indels
    8; Indels
  9; Mismatches
                                                                                                                                                                    61 DADKDGAVSFEEFVVLVSRVLKTAHIDIHK 90
                                                                                                                                     61 DANQDEQVSFKEFVVLVTDVLITAHDNIHK 90
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Patent No. 6670136
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Best Local Similarity 81.1
Matches 73; Conservative
Conservative
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Best Local Similarity
Matches 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Bovine
S-09-826-589-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Bovine
73;
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S-09-826-589-4
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Matches
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STRANDEDNESS:
TOPOLOGY: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-568-310D-2
          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
US-09-270-455-2
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1 Similarity 70.3%; Pred. No. 8.7e-33;
64; Conservative 10; Mismatches 17; Indels
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Patent No. 5976832
GENERAL INFORMATION:
APPLICANT: YAMAGUCHI, KEN
APPLICANT: YAMAGUCHI, KEN
APPLICANT: YAMAGUCHI, TATSUJI
TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
WUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE
                 APPLICANT: KIMURA, TATSUCI
TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: WYATT, GERBER, MELLER & O'ROURKE
STREET: 6th FLOOR
STREET: 6th FLOOR
CITY: NEW YORK CITY
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA PUBLICATION INFORMATION: RELEVANT RESIDUES IN SEQ ID NO: 20: FROM 1 TO 92
                                                                                                                                                                                                      COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE,3.50 INCH,720 Kb
MEDIUM TYPE: STORAGE
COMPUTER: IBM-PC COMPATIBLE
OPERATING SYSTEM: PC-DOS 6.2
SOFTWARE: WOLDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,455
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STREET: 99 PARK AVENUE
STREET: 6th FLOOR
CITY: NEW YORK CITY
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                                                                                                                                                                                                                                                                                                                                                                                                               TILING DATE:

CLASSIFTCATION: 435
PHIOR APPLICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NATA:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 27101
REPREBRENCE/DOCKET NUMBER: 3316
TELEPHONE: (212)953-3350
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
  YAMAMURA, TOKUJIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 64; Conservi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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APPLICANT:
APPLICANT:
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                                                                                     COMPUTER: IBM-PC COMPATIBLE
COMPUTER: BM-PC COMPATIBLE
OPERATING SYSTEM: PC-DOS 6.2
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/568,310D
FILING DATE: DECEMBER 6, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 7-70468 and 7-45564 (both Japan)
FILING DATE: 3/6/95 and 3/6/95, respectively
ATTORNEY AGENT INPORMATION:
NAME: KLEIN, MILTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: HITOMI, JIRO
APPLICANT: YAMAGUCHI, KEN
APPLICANT: YAMAGUCHI, KEN
APPLICANT: KMURA, TAKUJIRO
APPLICANT: KIMURA, TATSUJI
TITLE OF INVENTION: NOVEL CALCIUM-BINDING PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2:
FROM 1 TO 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: WYATT, GERBER, MELLER & O'ROURKE STREET: 99 PARK AVENUE STREET: 6th FLOOR STREET: 6th FLOOR STREET: NEW YORK CITY STATE: NEW YORK CITY COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE,3.50 INCH,720 Kb
MEDIUM TYPE: STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10016

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE,3.50 INCH,720 Kb
MEDIUM TYPE: STORAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/270,455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RELEVANT RESIDUES IN SEQ ID NO:
RELEVANT RESIDUES IN SEQ ID NO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/568,310
                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 27101
REFERENCE/DOCKET NUMBER: 3316
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)953-3350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09270455
Patent No. 6313267
GENERAL INFORMATION:
APPLICANT: HITOMI, JIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS 6.2
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212)953-3352
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212/500
TETERANE: (212)953-3352
THE TENEST (212)953-000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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Best Local Similarity
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APPLICANT: Siegenthaler, Georges
TITLE OF INVENTION: Isolated Arachidonic Acid-Binding Heteromer and its Use in
TITLE OF INVENTION: Cosmetics and Pharmaceutics
FILE REFERENCE: 016800-254
CURRENT APPLICATION NUMBER: US/09/214,272
CURRENT FILING DATE: 1999-04-09
PRIOR PLICATION NUMBER: PCT/FR97/01164
PRIOR FILING DATE: 1997-06-30
PRIOR FILING DATE: 1997-06-30
PRIOR FILING DATE: 1997-06-30
                                                                                                                              1 TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTL-KNTKDQGTIDKIFQN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTL-KNTKDQGTIDKIFQN 59
                                                                                                                                                           6 SQLBRNIETIINTFHQYSVKLGHPDTLNQGEFKELVRKDLNFLKKENKNEKVIEHIMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SQLERNIETIINTFHQYSVKLGHPDTLNQGEFKELVRKDLQNFLKKENKANEKVIEHIMED
                                                                                             Gaps
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Patent No. 5731166
GENERAL INFORMATION:
APPLICANT: Geczy, C., Simpson, R. J. and Lackmann, M
TITLE OF INVENTION: No. 5731166el Chemotactic Factor
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cushman Darby & Cushman
STREET: 1100 New York Avenue, N. W., Ninth Floor, East Tower
                                                                                             1,
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                                                  DB 1; Length 114;
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                                                                                           Indels
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45.1%; Pred. No. 2.3e-18;
tive 25; Mismatches 24;
                                                                                             24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Amino acid sequence of MRP-14.
US-09-214-272-4
                                                45.7%; Score 213.5; DB 1
45.1%; Pred. No. 2.3e-18;
iive 25; Mismatches 24
                                                                                                                                                                                                                   60 LDANQDEQVSFKEFVVLVTDVLITAHDNIHK 90
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
                                                                                                                                                                                                                                                                                                                                         US-09-214-272-4
; Sequence 4, Application US/09214272
; Patent No. 6620790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 114
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                                                                                         41; Conservative
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                                           Query Match
Best Local Similarity
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Best Local Similarity
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CITY: Wal
STATE: D
      US-08-385-241-3
                                                                                         Matches
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Patent No. 5776348
GENERAL INFORMATION:
APPLICANT: Selengut Ph.D., Jeremy D.
APPLICANT: Orme-Johnson Ph.D., William H.
APPLICANT: Draw-Lier M.D., Stephen P.
APPLICANT: Asakura M.D., Hirotaka
TITLE OF INVENTION: SYSTEM AND METHOD FOR INHIBITING
TITLE OF INVENTION: FORMATION OF CRYSTALLINE STRUCTURES THAT INCLUDE STRUVITE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/385,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   492611-000 (MIT6915)
                                                                                                                                                                                                                                                                                                                                                                                 50.3%; Score 235; DB 4; 90.0%; Pred. No. 2e-21; ive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Herschbach Ph.D., Brenda M.
REGISTRATION NUMBER: P-39,223
REFERENCE/DOCKET NUMBER: 492611-000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-5175
TELEPHONE: (617) 248-4000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Choate, Hall & Stewart
53 State Street
                                                                                                                                                                                                                                                                                                                 RELEVANT RESIDUES IN SEQ ID NO:
                                                                              REFERENCE/DOCKET NUMBER: 33
TELECOMNUNICATION INFORMATION:
TELEPHONE: (212)553-3350
TELEFAX: (212)953-3352
                                       NAME: KLEIN, MILTON
REGISTRATION NUMBER: 27101
                                                                                                                                           TELEFAX: (212)953-3352
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                          TOPOLOGY: linear PUBLICATION INFORMATION:
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Best Local Similarity
Matches 45; Conserv
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ZIP: 02109-2891
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MOLECULE TYPE: pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boston
                                                                                                                                                                                                                                                  STRANDEDNESS:
FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                       JS-09-270-455-2
                                                                                                                                                                                                         LENGTH:
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Sequence 2, Application US/09826589

Batent No. 6670136
GENERAL INFORMATION:
APPLICANT: Schmidt, Ann Marie
APPLICANT: Schmidt, Ann Marie
APPLICANT: Stern, David
TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THER)
FILE REFERENCE: 0575/58873-B-PCT-US
CURRENT APPLICATION NUMBER: US/09/826,589
CURRENT FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.1%; Score 206; DB 4; 82.0%; Pred. No. 6.3e-18; ative 3; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: March 5, 2004, 09:50:52 Job time: 23 secs
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; OTHER INFORMATION: x=any amino acid
US-09-826-589-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Human
                          -09-826-589-2
                                                                                                                                                                                                                                                                                                            LENGTH: 50
TYPE: PRT
                                                                                                                                                                                                                                                                                          SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                  FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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APPLICANT: Schmidt, Ann Marie
APPLICANT: Stern, David
TITLE OF INVENTION: Extracellular No. 6555340el RAGE Binding Protein (EN-RAGE) and
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 0575/55873-A
CURRENT APPLICATION NUMBER: US/09/263,312
CURRENT FILING DATE: 1999-03-05
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.3%; Score 211.5; DB 1; Length 109; 45.1%; Pred. No. 3.7e-18; tive 25; Mismatches 24; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.1%; Score 206; DB 4; Length 50; 82.0%; Pred. No. 6.3e-18; Live 3; Mismatches 6; Indels
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COTHER INFORMATION: Xaa at this position is unknown US-09-263-312-2
                                                                                                                                                                                                                                                                                    DWB/1925/200259
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APPLICATION NUMBER: US/07/987,272A
FILING DATE: 05-MAR-1993
CLASSIFICATION: 435
                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PK 2127
FILING DATE: 05-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PK 4463
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                     NAME: Brinkman, David W
REGISTRATION NUMBER: 20,817
REFERENCE/DOCKET NUMBER: DWB/TELECOMONICATION INFORMATION:
TELEPHONE: 202-861 3000
TELEPHONE: 202-821 0944
TELEX. 202-822 0944
TELEX. 6714627 CUSH
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          109 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 45.1%
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 82.0%
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-07-987-272A-8
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LENGTH: 50
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Sequence 3, Appli
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                                                                                                      5, 2004, 09:46:49 ; Search time 34 Seconds (without alignments) 565.145 Million cell updates/sec
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| cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/USO7_NEW PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-919-172-102
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US-09-826-589-4
US-09-872-185B-11
US-09-872-185B-12
US-10-077-600-2
US-10-134-841-4
US-10-136-279-32
US-10-116-275-225
US-10-116-275-225
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Maximum Match 100%
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17	178.5	æ	113	14	US-10-134-841-3	Sequence 3, Appli
18	171	9	91	14	US-10-106-698-6907	(U)
19	163	4	8	14	ᆏ	Sequence 1, Appli
20	163	4	101	σ	US-09-393-433-2	Segmence 2. Appli
21	163	4	101	on	-09-7	
22	163	34.9	101	14	US-10-269-643-2	Sequence 2, Appli
23	162	4	92	0	US-09-492-026-5	Sequence 5, Appli
24	162	4	92	0	US-09-919-039-184	Sequence 184, App
25	160	4	94	4	US-10-097-340-270	
26	159	4	68	4	US-10-316-253-46	Sequence 46, Appl
27	156	$\sim$	101		US-09-393-433-1	-
28	156	m	101	6	US-09-781-509-1	٦,
23	156	m	101	13	US-10-067-618-2	n)
30	156	3	101	13	US-10-135-152-2	'n
31	156	m	101	14	US-10-269-643-1	4
32	154	33.0	93	15	US-10-094-886-58	
33	151	N	93	14	841	7
34	151	$\alpha$	477	15	US-10-161-927-62	62
35	150	N	105	10	US-09-492-026-6	6
36	150		105	14	-10-097-340	272,
37	150	7	105	14	US-10-301-822-177	Sequence 177, App
38	150	$^{\circ}$	134	σι	US-09-925-302-694	94,
39	143	30.6	6	14	-10	Sequence 274, App
40	143	O	97	14	US-10-171-311-206	206
4.	143	0	97	15	-10-236	40,
42	4	0	84	10	-09-849-13	34
43	ċ	0	98		US-09-492-026-3	
44	140.5	30.1	110	15	-10-264-04	28
45	m	29.6	α	15	US-10-264-049-4104	Sequence 4104, Ap
					ALIGNMENTS	
RESULT						
US-09-8.	US-09-826-589-3					
; Segue:	Sequence 3, Application US/ Patent No. HS2002010672621	pplicati 20020106	on US/(	098265	6589	
	GENERAL INFORMATION	MATION:				
APPL	Οĵ		Ann Marie	ri e		
	APPLICANT: S	Stern, D	David			
FILE	TITLE OF INVENTION: EXTRACELLULAR N FILE REFERENCE: 0575/55873-B-PCT-HS	ENTION: CE: 0575	EXTRACT / 55873	31.10 - 8	OVEL RAGE BINDING	PROTEIN (EN-RAGE) AND USES
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US-09-826-589-3

Sequence 3, Application US/09826589

TILLE DE INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND US

TILLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND US

CURRENT APPLICATION NUMBER: US/09/826,589

CURRENT RILING DATE: 2001-04-05

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patentin version 3.1

SEQ ID NO 3

LENGTH: 90

TYPE: PRT

ORGANISM: Bovine

US-09-826-589-3

Query Match

Query Match

Query Match

TRIAN SEQUENCE 366; DB 9; Length 90;

Best Local Similarity 81.1%; Pred. No. 1.2e-32;

Matches 73; Conservative 9; Mismatches, 8; Indels 0; Gaps 0;
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; Sequence 4, Application US/09826589; Patent No. US20020106726Al; GENERAL INFORMATION: APPLICANT: Schmidt, Ann Maxie

US-09-826-589-4

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Sequence 2, Application US/10077600

Bublication No. US20030175713A1

GENERAL INFORMATION:
APPLICANT: Switch Biotech AG

TITLE OF INVENTION: Method for diagnosis of inflammatory diseases using Calgranulin (
URRENT APPLICATION NUMBER: US/10/077,600

CURRENT FILING DATE: 2002-06-14

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: HALLE, JORN-PETER
APPLICANT: HALLE, JORN-PETER
APPLICANT: GOPPELT, ANDREAS
TITLE OF INVENTION: MRPS/MRP14 heterodimer, or its
TITLE OF INVENTION: individual components in combination, for treating and/or
TITLE OF INVENTION: preventing skin diseases, wounds and/or wound-healing
TITLE OF INVENTION: disturbances, having a reduced quantity of MRPS/MRP14
FILE REPERENCE: 50125/031002
CURRENT APPLICATION NUMBER: US/10/134,841
CURRENT FILING DATE: 2002-04-29
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Pred. No. 1.2e-32;
9; Mismatches 8; Indels
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           US/09/872,185B
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PRIOR FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: DE 10121254.2
PRIOR FILING DATE: 2001-04-30
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Publication No. US20030003482A1
       CURRENT APPLICATION NUMBER: US/0
CURRENT FILING DATE: 2001-06-01
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATENTIN VERSION 3.1
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81.1%;
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Best Local Similarity 81.1:
Matches 73; Conservative
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Best Local Similarity 70.3%
64; Conservative
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LENGTH: 90
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                     TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERE THE REPRENDENCE: 0575/55803-3-PCT-US
CURRENT APPLICATION NUMBER: US/09/826,589
CURRENT FILING DATE: 2001-04-05
SOFTWARE: PACOLIN VOS: 6
SOFTWARE: Pacolin version 3.1
SEQ ID NO 4
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81.1%; Pred. No. 1.2e-32;
ive 9; Mismatches 8; Indels
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APPLICANT: Stern, David M.
APPLICANT: Tan, Shi Du
APPLICANT: Yan, Shi Du
APPLICANT: Lamster, Ira
TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
FILE REPRENCE: 0575/64080
CURRENT APPLICATION WIMBER: US/09/872,185B
CURRENT FILING DATE: 2001-06-01
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APPLICANT: Herold, Kevan
APPLICANT: Yan, Shi Du
APPLICANT: Schmidt, Ann Marie
APPLICANT: Lamster, Ira
TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
FILE REFERENCE: 0575/64080
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Pred. No. 1.2e-32;
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; Patent No. US20020122799A1
; GENERAL INFORMATION:
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Best Local Similarity 81.1%;
Matches 73; Conservative
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SOFTWARE: PatentIn version 3.1
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Best Local Similarity 81.1%;
Matches 73; Conservative
    Stern, David
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ORGANISM: Bovine
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US-09-872-185B-11
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LENGTH: 90
APPLICANT:
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Sequence 2, Application US/09826589
Patent No. US20020106726A1
GENERAL INFORMATION:
APPLICANT: Schmidt, Ann Marie
APPLICANT: Schmidt, Ann Marie
TILLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND USES THERER FILE REFERENCE: 0575/55873-B-PCT-US
CURRENT APPLICATION NUMBER: US/09/826,589
CURRENT FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 146, Application US/10131410

Sequence 146, Application No. US2003023591541

GENERAL INCORMATION:

APPLICANT: SPECHT, THOMAS

APPLICANT: HINZMANN, BERND

APPLICANT: PILARSKY, CHRISTIAN

APPLICANT: PILARSKY, CHRISTIAN

APPLICANT: DAHL, EDGAR

TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM TISSUE OF BREAST

TITLE OF INVENTION: TUMON NUCLEIC ACID SEQUENCES FROM TISSUE OF BREAST

TITLE OF INVENTION: TUMON NUCLEIC ACID SEQUENCES

FILER REFERENCE: SCH-1763

CURRENT APPLICATION NUMBER: US/10/131,410

CURRENT FILING DATE: 2002-04-25

PRIOR APPLICATION NUMBER: 09/646,673

PRIOR APPLICATION NUMBER: PCT/DE99/00908

PRIOR FILING DATE: 1999-03-19

NUMBER OF SEQ ID NOS: 202
                                                                                                                                                                                                                                                             1 TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTL-KNTKDQGTIDKIFQN 59
                                                                                                                                                                                                                                                                                            6 SQLERNIETIINTFHQYSVKLGHPDTLNQGEFKELVRKDLQNFLKKENKNEKVIEHIMED 65
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Best Local Similarity 45.1%; Pred. No. 7.7e-16;
Matches 41; Conservative 25; Mismatches 24;
                                                                                                                                                       45.7%; Score 213.5; DB 15
45.1%; Pred. No. 7.7e-16;
tive 25; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                               60 LDANQDEQVSFKEFVVLVTDVLITAHDNIHK 90
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                                                                                                                                                          Query Match
Best Local Similarity 45.19
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 146
LENGTH: 114
                       ; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-275-225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT; ORGANISM: Homo sapiens
US-10-131-410-146
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US-10-131-410-146
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US-09-826-589-2
       SEQ ID NO 225
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'S-10-308-279-32
Squence 32, Application US/10308279
Publication No. US20030170742A1
GENERAL INFORMATION:
GENERAL INFORMATION:
FIGURE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/308,279
CURRENT FILING DATE: 2002-12-03
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 91
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: O'Mahony, Daniel J.
APPLICANT: Brayden, David
APPLICANT: Brayden, David
APPLICANT: Byrne, David
APPLICANT: Lambkin, Imelda
APPLICANT: Lambkin, Inelda
APPLICANT: Higgins, Lisa
APPLICANT: Higgins, Lisa
APPLICANT: Higgins, Lisa
APPLICANT: Compositions Targeting Peyer's Patches and M Cells and Methods and
TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
FILE REFERENCE: B1067/20087
FILE REFERENCE: B1067/20087
FILE CURRENT APPLICATION UNDER: US/10/116,275
CURRENT FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 349
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                                                                                                                                                                                                   45.7%; Score 213.5; DB 1.45.1%; Pred. No. 7.7e-16;
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NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 114
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PAPLICANT: O'Mahony, Daniel J.
APPLICANT: Brayden, David
APPLICANT: Byrne, Daragh
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Publication No. US20030211476A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                          41; Conservative
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ORGANISM: homo sapiens
                                                                                                                          ORGANISM: Homo sapien
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Best Local Similarity
Matches 41; Conserva
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Matches 41; Conserv
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S-10-116-275-225
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                                                                                                                                                    S-10-134-841-4
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                                                                                                   TYPE: PRT
                                                                                                                                                                                                         Query Match
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SOFTWARE:
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ADDRESSEE: Incyte Ph
STREET: 3174 Porter
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41.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94304
COMPUTER READABLE FORM:
                         TYPE: PRT ORGANISM: Rattus norvegicus
                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY: GenBank
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Palo Alto
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Best Local Similarity
Matches 38; Conserv
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Best Local Similarity
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US-09-492-026-7
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                                                                      FEATURE:
          LENGTH:
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APPLICANT: Dixon, Alistair
APPLICANT: Brooksbank, Robert
APPLICANT: Brooksbank, Robert
TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
FILE REFERENCE: WL-A-018200
CURRENT APPLICATION NUMBER: US/10/205,219
FILE REPEATOATION NUMBER: GB 0118354.0
PRIOR APPLICATION NUMBER: GB 0118354.0
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 197
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 161
                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                              Score 206; DB 9; Length 50;
Pred. No. 1.9e-15;
3; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/09872185B
Patent No. US20020122799A1
GENERAL INFORMATION:
APPLICANT: Stern, David M.
APPLICANT: Aren, Shi Du
APPLICANT: Aren, Shi Du
APPLICANT: Aren, Shi Du
APPLICANT: Isamster, Ira
ITILE OF INVENTION: METHODS FOR TREATING INFLAMMATION
FILE REFERENCE: 055764080
CURRENT APPLICANION NUMBER: US/09/872,185B
CURRENT APLING DATE: 2001-06-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (47) ... (47)
OTHER INFORMATION: Where Xaa = unknown
                                                                            FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (47)...(47)
COTHER INFORMATION: x=any amino acid
US-09-826-589-2
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Publication No. US20030138803A1
GENERAL INFORMATION:
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                                                                                                                                                                                                          Query Match
Best Local Similarity 82.0%;
Matches 41; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lee, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Bovine
                                          TYPE: PRT
ORGANISM: Human
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SEQ ID NO 2
LENGTH: 50
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1 TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTK-DQGTIDKIFQN 59
                                                                                                               Gaps
                                                                                                             7;
                                                              43.8%; Score 204.5; DB 14; Length 112;
41.8%; Pred. No. 7.3e-15;
Live 24; Mismatches 28; Indels 1;
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; OTHER INFORMATION: Intracellular calcium binding protein US-10-205-219-161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 204.5; DB 1 Pred. No. 7.4e-15;
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                                                                                                                                                                                                                                          60 LDANQDEQVSFKEFVVLVTDVLITAHDNIHK 90
                                                                                                                                                                                                                                                                  67 LDTNQDNQLSFEECMMLMGKLIFACHEKLHE 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lal, Preeti
Shah, Purvi
TITLE OF INVENTION: HUMAN S100 PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/492,026A
FILING DATE: 26-Jan-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/09492026A
Publication No. US20030096337A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer I
Bandman, Olga
Corley, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Colette C. Muenzen
REGISTRATION NUMBER: 39,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
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Gaps

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1 TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTKDQGTIDKIFQNL
EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
EXPRESSED IN BRAIN, SIGNAL = 1.2
EXPRESSED IN BONE MARROW, SIGNAL = 7.1
EST HUMAN HIT: AVV15719.1, EVALUE 1.00e-19
SWIŠSPROT HIT: PRO511, EVALUE 1.00e-20
                                                                                                                                                                                                                         41.1%; Score 192; DB 9; Length 46; 80.0%; Pred. No. 5.7e-14; rative 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020119463A1 1422432CD1
                                                                                                                                                                                                                                                                                                                                                                                               2 TKLBEHLEGIVNIFHQYSVRKGHFDTLSKGELKQLLTKELANTIK 46
                                                                                                                                                                                                                                                                                                                                                     1 TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLK 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 38.8%; Score 181; DB 9; Length 95 Best Local Similarity 43.3%; Pred. No. 2.2e-12; Matches 39; Conservative 15; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 DANQDEQVSFKEFVVLVTDVLITAHDNIHK 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Turner, Christopher M.
TITLE OF INVENTION: PROSTATE CANCER MARKERS
FILE REFERENCE: PA-0036 US
CURRENT APPLICATION NUMBER: US/09/919,172
CURRENT FILING DATE: 2001-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DANGDAQVDFSEFIVFVAAITSACHKYFEK 91
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PRIOR APPLICATION NUMBER: 60/222,469
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PERL PROGRAM
SO ID NO 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 102, Application US/09919172
Patent No. US20020119463A1
GENERAL INFORMATION:
APPLICANT: Faris, Mary
APPLICANT: Turner, Christopher M.
                                                                                                                                                                                                               Query Match
Best Local Similarity 80.0°
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                               OTHER INFORMATION: E
COTHER INFORMATION: E
COTHER INFORMATION: E
COTHER INFORMATION: C
US-09-864-761-41579
      OTHER INFORMATION:
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LENGTH: 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
                                                            1 TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTK-DQGTIDKIFQN 59
                                                                                            1; Gaps
   28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEATURE:
OTHER INFORMATION: MAP TO ACO11666.18
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILER REFERENCE: AGONGGE-X-I CURRENT APPLICATION: GGENE EXPRESSION ANALYSIS BY MICROR CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-09-03
PRIOR PLING DATE: 2000-09-03
PRIOR PLING DATE: 2000-09-03
PRIOR PLING DATE: 2000-09-07
PRIOR PLING DATE: 2000-09-07
PRIOR PELING DATE: 2000-09-07
PRIOR PELING DATE: 2000-09-07
PRIOR PREDICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PR
24; Mismatches
                                                                                                                                                                                  60 LDANQDEQVSFKEFVVLVTDVLITAHDNIHK 90
                                                                                                                                                                                                                      67 LDTNQDNQLSFEECMMLMGKLIFACHEKLHE 97
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 41579, Application US/09864761 Patent No. US20020048763A1
38; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION
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Matches
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Length 95;

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                    Copyright
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- protein search, using sw model M protein 5, 2004, 09:43:38; Search time 20 Seconds (without alignments) 437.671 Million cell updates/sec March uo un;

itle:

1 TKLEDHLEGIINIFHQYSVR......EFVVLVTDVLITAHDNIHKE US-09-646-651C-1 467 erfect score:

**BLOSUM62** coring table: sednence:

Gapop 10.0 , Gapext 0.5

283366 seqs, 96191526 residues earched:

hits satisfying chosen parameters: otal number of

linimum DB seq length: 0 faximum DB seq length: 2000000000

Listing first 45 summaries Ost-processing: Minimum Match 0% Maximum Match 100%

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* atabase:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		*				
tesult No.	Score	Query Match	Length	DB	ID	scription
	467		91	2	A55406	algranulin c
7	332	ä	92	~	JC4712	-
М	$\overline{}$	•	122		A42628	granulin
4	213.5	45.7	114	Н	B31848	granulin B [v
2	4	٠	113	Н	JN0686	algranulin B -
9	181	38.8	95	N	S24146	00 protein P
7	178.5	œ,	113	Н	S68242	algranulin B
œ	167		95		S35985	S-100 protein alph
σ	164	35.1	92	2	A26557	-100 protein
10	163	4.	89	Н	I56163	algranulin A
11	163	•	16	Н	BCBOIB	S-100 protein beta
12	163		92	N	A48015	-100 protein
13	163	34.9	101	N	806207	alvas
14	162		92		BCHUIB	-100 protein
15	161	4.	94	Н	BCBOIA	
16	160		94	Н	BCHUIA	-100
17	160	34.3	101	N	801759	1
18	159	•	89	-4	JN0685	calgranulin A - ra
19	156	ω,	101	N	A48219	calvasculin - huma
20	154	33.0	102	Н	JQ1300	calgizzarin - rabb
21	153	•	100	~	A53217	placental calcium-
22	151	•	93	Н	BCHUCF	calgranulin A [val
23	151	'n.	591	(1)	A45135	profilaggrin - hum
24	150	ς.	105	-	I37080	calgizzarin - huma
25	148	•	96	~	A41988	
26	147	31.5	306	7	A48118	major epidermal ca
27			79	Н	KLPGI	
28		0	110	N	B48219	
29	40.	30.1	86	7	JC5064	-10

calcium-binding pr	S-100 protein, lun	calcyclin - human	calpactin I light	calcium-binding pr	calcyclin - rabbit	calpactin I light	calpactin I light	calcium-binding pr	calcyclin - mouse	calpactin I light	calpactin I light	calpactin I light	calcyclin - rat	26-kDa Ca2+-bindin	calcium-binding pr
JN0246	A30129	BCHUY	A28489	KLBOI	S27011	A31373	JH0663	S20342	A54314	LUPG10	JC1139	B28489	B28363	JE0330	JC5065
н	7	Н	7	-1	Н	7	Н	~	7	Н	N	~	~	2	7
79	97	90	97	79	90	95	97	66	8	95	97	97	90	217	98
29.9	29.6	29.1	29.0	28.9	28.9	28.8	28.6	28.5	28.1	27.7	27.7	27.7	27.4	27.3	26.9
139.5 29.9	138 29.6	136 29.1	135.5 29.0	135 28.9		134.5 28.8				129.5 27.7				127.5 27.3	

## ALIGNMENTS

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calgranulin c - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Accession: A55406
R;Dell'Angelica, E.C.; Schleicher, C.H.; Santome, J.A.
J;Biol. Cham. 269, 28929-28936, 1994
A;Fible: Primary structure and binding properties of calgranulin C, a novel S100-like ca A;Reference number: A55406; MUID:95050708; PMID:7961855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTKDQGTIDKIFQNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                   Length 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                       A;Accession: A55406
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-91 -02E.>
C;Superfamily: S-100 protein; calmodulin repeat homology
C;Keywords: calcium binding; EF hand
F;48-80/Domain: calmodulin repeat homology <EF2>
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 467; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.6e-37;
Matches 91; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 DANODEOVSFKEFVVLVTDVLITAHDNIHKE 91
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S-100 calcium-binding protein A12 - human N;Alternate names: calcium-binding amniotic fluid protein 1 (CAAF1); calgranulin C; calg

E.; Saito, S.; Tsukada,

utrophil protein
() Species: Home sapiens (man)
() Species: Home sapiens (man)
() Species: Home sapiens
() Accession: UC4712, UC4717, UC4891, S56113, S56114
() Accession: UC4712, UC4717, UC4891, S56113, S56114
() Armamura, T.; Hitomi, U.; Nagasaki, K.; Suzuki, M.; Takahashi, E.; Saito, S.; Tsukadi Biochem. Biophys. Res. Commun. 221, 356-360, 1996
() A; Title: Human CAAPI gene - molecular cloning, gene structure, and chromosome mapping.
() A; Reference number: UC4712; MUD: 96192053; PMID: 8619860

A;Accession: JC4712 A;Molecule type: mRNA A;Residues: 1-92 <YAM>

A)Cross-references: DDBJ:DB3657; NID:g1502284; PIDN:BAA12030.1; PID:g1502285
R;Marti, T.; Erttmann, K.D.; Gallin, M.Y.
Biochem. Biochys. Res. Commun. 221, 454-458, 1996
A;Title: Host-parasite interaction in human onchocerciasis: Identification and sequence A;Reference number: JC4717; MUID:96192069; PMID:8619876

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calgranulin B [validated] - human
N;Alternate names: calcium-binding protein MRP-14; cystic fibrosis-associated antigen (
(MRP-14); MIF-related 14K protein; S-100 calcium-binding protein A9 (S100A9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-114 <MUR>
A;Residues: 1-114 <MUR>
A;Cross-references: GB:M26311; NID:g862619; PIDN:AAA68480.1; PID:g516621
A;Note: part of this sequence was confirmed by protein sequencing; the amino end of the R;Noterspon, K.B.; Sletten, K.; Berntzen, H.B.; Dale, I.; Brandtzaeg, P.; Jellum, E.; F; Scand. J. Immunol. 28, 241-245, 1988
A;Fitle: The leucocyte L1 protein: identity with the cystic fibrosis antigen and the call A;Reference number: A60911; MUID:88321575; PMID:3413449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: protein
A;Residues: 5-77;80-90,'A',92-114 <TOB>
A;Note: the blocked amino end of the mature protein is identified as 2-Thr; residue 91-1
R;Madsen, P.; Rasmussen, H.H.; Leffers, H.; Honore, B.; Dejgaard, K.; Olsen, E.; Kill,
                                        hand; heterodimer; inflammation; pho:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Title: Cloning and expression of two human genes encoding calcium-binding proteins the A,Reference number: A93102; WUID:88302148; PMID:3405210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: A protein containing the cystic fibrosis antigen is an inhibitor of protein kir A;Reference number: A33819; MUID:89255276; PMID:2656677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 39-42, X',44-50;64-77, X',79;84,'X',86-90,'X',92-94,'X',96-98 <AND>
R;Tobe, T.; Murakami, K.; Tomita, M.; Nozawa, R.
Chem. Pharm. Bull. 37, 1276-1380, 1989
A;Title: Amino acid sequences of 6088 antigens induced in HL-60 cells by 1,25-dihydroxyr
A;Reference number: A61082; MUID:89376538; PMID:2776242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Residues: 1-114 < LAG>
A, Cross-references: GB:M21064; NID:g188689; PIDN:AAA36326.1; PID:g386958
R;Odink, K.; Cerletti, N.; Brueggen, J.; Clerc, R.G.; Tarcsay, L.; Zwadlo, G.; Gerhards Nature 330, 80-82, 1987
A, Title: Two calcium-binding proteins in infiltrate macrophages of rheumatoid arthritis A, Reference number: S00667; MJID:88039099; PMID:3313057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and expression of a novel partially secreted pro
                                                                                                                                                                                                                                                                                                                                1 TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTL-KNTKDQGTIDKIFQN 59
                                                                                                                                                                                                                                                                                                                                                                                                      SOMESSIETIINIFHQYSVRLGHYDTLIQKESKÖLVQKELPNFLKKQKKNEAAINEIMED 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.Species: Homo sapiens (man)
C.Date: 21-May-1990 #sequence_revision 23-May-1997 #text_change 08-Dec-2000
C.Accession: B31848; S00667; A33819; B60911; B61082; D54327
                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                          Length 122;
                                                                                                                                                                                                                                                             18; Indels
   C, Superfamily: S-100 protein; calmodulin repeat homology C, Keywords: blocked amino end; calcium binding; EF hand; F; 6-40/Domain: calmodulin repeat homology < BF1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Title: Molecular cloning, occurrence, and expression of A, Reference number: A54327; MUID:92043866; PMID:1940442
                                                                                                                                                                                          DB 1;
                                                                                                                                                                                  56.0%; Score 261.5; DB 1 ilarity 53.3%; Pred. No. 6.6e-18; Conservative 23; Mismatches 18
                                                                          F;50-82/Domain: calmodulin repeat homology <BF2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 LDANQDEQVSFKEFVVLVTDVLITAHDNIH 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Invest. Dermatol. 97, 701-712, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Lagasse, E.; Clerc, R.G.
Mol. Cell. Biol. 8, 2402-2410, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
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N;Alternate names: calcium-binding protein MRP-14; macrophage migration inhibitory facto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R,Dianoux, A.C.; Stasia, M.J.; Garin, J.; Gagnon, J.; Vignais, P.V.
Biochemistry 31, 5898-5905, 1992
A;Title: The 23-kilodalton protein, a substrate of protein kinase C, in bovine neutrophi
A;Reference number: A42628; MUID:92304974; PMID:1610833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Comment: This protein is released by activated neutrophils in the course of inflammatd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1993 #sequence_revision 23-May-1997 #text_change 23-May-1997
C;Date: 30-Sep-1993 #sequence_revision 23-May-1997
C;Accession: B22309; A42628
R;Tang, T.K.; Hong, T.M.; Lin, C.Y.; Lai, M.L.; Liu, C.H.L.; Lo, H.J.; Wang, M.E.; Chen, submitted to the Protein Sequence Database, July 1992
A;Reference number: A22309
                                                                                                           R;llg, B.C.; Troxler, H.; Buergisser, D.M.; Kuster, T.; Markert, M.; Guignard, F.; Hunzi
Biochem. Bloghys. Res. Commun. 225, 146-150, 1996
A;Hitle: Amino acid sequence determination of human 5100 Al2 (P6, Calgranulin C, CGRP, C
A;Reference number: UC4891; MUID:96332419; PMID:8769108
                                                                                                                                                                                                                                                                                                                                                                                                                                            novel human neutrophil protein related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 TKLEEHLEGIVNIFHQYSVRKGHFDTLSKGELKQLLTKELANTIKNIKDKAVIDEIFQGL
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A;Nolecule type: protein
A;Residues: 2-92 <MAR>
A;Experimental source: Onchocerca volvulus infecting human tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.1%; Score 332; DB 2; Length 92; 70.3%; Pred. No. 1e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17; Indels
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A,Residues: 4-32,'F',34-56 <DIA>
C;Complex: heterodimer and higher complexes with calgranulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Superfamily: S-100 protein; calmodulin repeat homology
                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Residues: 2-92 <ILG>
R; Guignard, F:; Mauel, J:; Markert, M.
Biochem. J. 309, 395-401, 1995
A; Title: Identification and characterization of a novel
A; Reference number: S56113; MUID:95351965; PMID:7626002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Pred. No. 1e-24; 10; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: GDB:S100A12; p6; MRP6; CGRP; CAAF1
A;Cross-references: GDB:5218374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: protein
A;Residues: 'XX',4-14,'X',16-17,'XXXX'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Residues: 2-21 <GUI2>
A;Experimental source: isoform 6b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: isoform 6a
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C; Complex: monomer
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A,Status: preliminary
A,Molecule type: protein
A;Residues: 1-122 <TAN>
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Matches 64; Conserv
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A; Status: preliminary
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Query Match

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 $\delta$ d A42628

C.Genetics:

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Calgranulin B - mouse

NyAlternate names: calcium-binding protein MRP-14; macrophage migration inhibitory facto
C;Species: Mus musculus (house mouse)
C;Date: 06-Sep-1996 #sequence_revision 23-May-1997 #text_change 22-Jun-1999
C;Accession: S68242; S68272
R;Lagasse, B.; Watssman, I.L.
R;Lagasse, B.; Watssman, I.L.
A;Description: Mouse MRPS and MRP14, two intracellular calcium-binding proteins associat
A;Reference number: S68242
                                                                                                                                                                                                                                                                                        human placenta. cDNA cloning, recomb
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A;Note: 107-His is identified as 3'-methylhistidine; the authors' source for the referen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Title: Isolation of the murine S100 protein MRP14 (14 kDa migration-inhibitory-factor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the S-100 protein family
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    S-100 protein P - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
C;Accession: S24146; Ps0340
R;Becker, T.; Gerke, V.; Kube, E.; Weber, K.
Bir. J. Biochem. 207, 541-547, 1992
A;Title: S100P, a novel Ca(2+)-binding protein from human placenta. cDNA clc A;Reference number: S24146; MUID:92339442; PMID:1633809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTKDQGTIDKIFQNL
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R;Raftery, M.J.; Harrison, C.A.; Alewood, P.; Jones, A.; Geczy, C.L.
Biochem. J. 316, 285-293, 1996
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A/Molecule type: mRNA
A/Residues: 19e1Iminary
A/Rosereferences: BMBL:X65614; NID:g36177; PIDN:CAA46566.1; PID:g36178
A/Cross-references: BMBL:X65614; NID:g36177; PIDN:CAA46566.1; PID:g36178
B/Status: 1.246.1253, 1992
B/A/Cross-reference number: Res. Commun. 182, 1246.1253, 1992
A/Reference number: PS0340; MUID:92171935; PMID:1540168
A/Recession: PS0340
A/Rocession: PS0340
A/Residues: 1.31, 'T, 33-84, 'X', 86-91 < BMO>
A/Gene: GDB:S100P
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38.8%; Score 181; DB 2;
Best Local Similarity 43.3%; Pred. No. 2.1e-10;
Matches 39; Conservative 15; Mismatches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: S-100 protein; calmodulin repeat PC;Keywords: calcium binding; EF hand; placenta F;6-40/Domain: calmodulin repeat homology <EF1>F;49-81/Domain: calmodulin repeat homology <EF2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GDB:134405; OMIM: 600614
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A; Residues: 2-10;95-109 <RAF>
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A;Residues: 1-113 <LAG>
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'I. Manichi, T.; Uchida, I.; Wahl, S.M.; McCartney-Francis, N.
siochem. Biophys. Res. Commun. 194, 819-825, 1993
'Jitle: Expression and cloning of migration inhibitory factor-related protein (MRP)8 an
Residues: 11-19,26-38;94-105, X',107 <MAD>
Note: in several peptide samples no PTH was detected for 95-His but in one peptide PTH (Comment: This protein appears to be expressed only in cells of myeloid origin actively (Comment: The presence of 3'-methylhistidine at position 105, corresponding to 107-His
                                                                                                                                                                                                                                                                                                                                                                                                        Note: the first intron occurs before the initiator codon (see PIR:BCHUCF)
;Complex: heterodimer and higher complexes with calgranulin A (see PIR:BCHUCF)
;Superfamily: $-100 protein; calmodulin repeat homology
;Keywords: blocked amino end; calcium binding; BF hand; heterodimer; inflammation; phos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (probably acetylated) #statu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complex: heterodimer and higher complexes with calgranulin A. Suberfamily: S-100 protein; calmodulin repeat homology (**Suberfamily: S-100 protein; calmodulin repeat homology (**Suberfamily: S-113/Product: catgranulin B #status predicted <MAT> (**)11-45/Domain: calmodulin repeat homology <EF1> (**)11-45/Domain: calmodulin repeat homology <EF2> (**)20-40 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)20 % (**)2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQLERNIETIINTFHQYSVKLGHPDTLNQGEFKELVRKDLQNFLKKENRONEKVIEHIMED 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SQLERSISTIINVFHQYSRKYGHPDTLNKABFKEMVNKDLPNFLKREKRHENLLRDIMED 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTK-DQGTIDKIFQN 59
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;Date: 03-May-1994 #sequence_revision 23-May-1997 #text_change 22-Jun-1999
                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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.,Residues: 1-113 <IMA>
./Cross-references: GB:L18948; NID:G488156; PIDN:AAA18214.1; PID:g488157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;10-44/Domain: calmodulin repeat homology <EF1>;54-86/Domain: calmodulin repeat homology <EF2>;2/Modified site: blocked amino end (Thr) (in mature form) (prok;113/Binding site: phosphate (Thr) (covalent) #status predicted
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45.7%; Score 213.5; DB 1; 45.1%; Pred. No. 2.1e-13; tive 25; Mismatches 24;

Query Match
Best Local Similarity 45.1
Matches 41; Conservative

LDANQDEQVSFKEFVVLVTDVLITAHDNIHK 90 

9

ă × ď algranulin B - rat

0.00686

Accession: JN0686

Gene: MRP14

Genetics:

67 LDTNQDNQLSFEECMMLMGKLIFACHEKLHE 97

9

ESULT

60 LDANQDEQVSFKEFVVLVTDVLITAHDNIHK 90

41.8%; Prec. No.

Query Match
Best Local Similarity 41.8
Matches 38; Conservative

..

Gaps

38; Indels

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A;Cross-references: EMBL:X01090; NID:g57174; PIDN:CAA25567.1; PID:g57175
R;Dunn, R.; Landry, C.; O'Hanlon, D.; Dunn, J.; Allore, R.; Brown, I.; Marks, A.
J. Biol. Chem. 262, 3562-3566, 1987
A.Title: Reduction in S100 protein Beta-subunit mRNA in C6 rat glioma cells following A;Reference number: A26557; MUID:87137648; PMID:3818655
                                                                                                                                                                                                                                                                                                 C; Comment: S-100 protein occurs as alpha-beta heterodimers, alpha-alpha heterodimers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 SELEKAMVALIDVFHQYSGREGDKHKLKKKSELKELINNELSHFLEEIKEQEVVDKVMETL
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                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: S-100 protein; calmodulin repeat homology
C;Keywords: brain; calcium binding; dimer; EF hand; zinc
E;2-92/Product: S-100 protein beta chain #status predicted <MAT>
F;6-40/Domain: calmodulin repeat homology <EF1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 164; DB 2;
Pred. No. 8.2e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 DANODEOVSFKEFVVLVTDVLITAHDNIHKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 37.4%
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 33.08
Matches 30; Conservative
                                                                                                                                                                                                                                                                          A; Cross-references: GB:M15705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein A;Residues: 2-77 <LAC2>
                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 6-92 < DUN>
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                                                                                                                                                                                                                                                                                                                                                            A; Introns: 46/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
                                                                                                                                                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
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R.Kuwano, R.; Usui, H.; Maeda, T.; Fukui, T.; Yamanari, N.; Ohtsuka, E.; Ikehara, M.; Ta
Nucleic Acids Res. 12, 7455-7465, 1984
A;Title: Molecular cloning and the complete nucleotide sequence of cDNA to mRNA for S-16
A;Reference number: S07357; MUID:85037924; PMID:6093041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            岩
        C;Keywords: acetylated amino end; calcium binding; EF hand; heterodimer; inflammation; F:12-113/Product: calgranulin B #status predicted <MAT>
F:11-45/Domain: calmodulin repeat homology <AFF>>
F:55-87/Domain: calmodulin repeat homology <AFF>>
F:55-87/Domain: calmodulin repeat homology <AFF>>
F:2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental F:103,105:101fied bonds: #status experimental F:103,105.107/Binding site: zinc (His) #status predicted F:107/Modified site: 3'-methylhistidine (His) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eggs; identification of
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335965
S-100 protein alpha chain - weatherfish
C;Species: Misgurnus fossilis (weatherfish)
C;Species: Misgurnus fossilis (weatherfish)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S35985
R;Ivanenkov, V.V.; Gerke, V.; Minin, A.A.; Plessmann, U.; Weber, K.
Mech. Dev. 42, 151-158, 1993
A;Title: Transduction of Ca(2+) signals upon fertilization of eggs; identifi
A;Accession: S35985; MUID:94031845; PMID:8217841
A;Accession: S35985
A;Molecule type: protein
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                                                                                                                                                                                                                                                                                                                                                                                          1 TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTK-DQGTIDKIFQN
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                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                       Query Match 38.2%; Score 178.5; DB 1; Length 113; Best Local Similarity 36.3%; Pred. No. 4.4e-10; Matches 33; Conservative 27; Mismatches 30; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.8%; Score 167; DB 1; Length 95; 40.7%; Pred. No. 4.4e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Residues: 1-95 <1VA>
C, Superfamily: S-100 protein; calmodulin repeat homology
C, Keywords: calcium binding; EF hand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LDANQDEQVSFKEFVVLVTDVLITAHDNIHK 90
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C;Species: Rattus norvegicus (Norway rat)
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Best Local Similarity
Matches 35; Conserv
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A; Residues: 1-92 <MAE>
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A; Residues: 1-89 <LAC1>
A; Residues: 1-89 <LAC1>
A; Cross-references: GB:S57123; NID:g298706; PIDN:AAB25840.1; PID:g298707
A; Cross-references: GB:S57123; NID:g298706; PIDN:AAB25840.1; PID:g298707
B; Lackmann, M.; Cornish, C.J.; Simpson, R.J.; Moritz, R.L.; Geczy, C.L.
J. Biol. Chem. 267, 7499-7504, 1992
A; Title: Purification and structural analysis of a murine chemotactic cytokine (CP-10) A; Reference number: A42488; MUID:92218405; PMID:1559987
        macrophage
                                                                                                                                                                  Rilackmann, M.; Rajāsekariah, P.; Iismaa, S.E.; Jones, G.; Cornish, C.J.; Hu, S.; Simps:
J. Immunol. 150, 2981-2991, 1999
A.Title: Identification of a chemotactic domain of the pro-inflammatory S100 protein CP
A.Reference number: 156163; MUID:93203618; PMID:8454868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Gene: MRP8
C;Complex: homodimer; heterodimer and higher complexes with calgranulin B
C;Superfamily: S-100 protein; calmodulin repeat homology
C;Reywords: calcium binding; cytokine; EF hand; heterodimer; homodimer; inflammation
F;2-89/Product: calgranulin A #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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N;Alternate names: calcium-binding protein MRP-8; CP-10 chemotactic protein; C;Species: Mus musculus (house mouse)
C;Date: 26-Jul-1996 #sequence_revision 23-May-1997 #text_change 22-Jun-1999
C;Accession: I56163; A42488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTKDQGTIDKIFQNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence extracted from NCBI backbone (NCBIP:94068)
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                                                                                                                                                                                                                                                                                                                                                                      A, Status: preliminary; translated from GB/EMBL/DDBJ
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F;46-78/Domain: calmodulin repeat homology <EF2>
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S-100 protein beta chain - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Os-Jun-1995 #sequence_revision 02-Jun-1995 #text_change.24-Nov-1999
C;Accession: A48015
R;Jiang, H.; Shah, S.; Hilt, D.C.
J. Biol. Chem. 268, 20502-20511, 1993
A;Title: Organization, sequence, and expression of the murine Sl00beta gene. Transcripti
A;Reference number: A48015; MUID:93388628; PMID:8376406
A;Reference number: A48015
A;Accession: A48016
A;Accession: A48016
A;Accession: A48016
A;Accession: A48016
A;Accession: A48016
A;Accession: A48016
A;Accession: A48
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C;Species: J1-bec-1990 #sequence revision 31-bec-1990 #text change 20-Jun-2000
C;Accession: S06207; JH0097; S07991; A26803; A41411; I48674
R;Ebralideze, A.; Tulchinsky, E.; Grigorian, M.; Afanasyeva, A.; Senin, V.; Revazova, E.; A;Tulchinsky, E.; Grigorian, M.; Afanasyeva, A.; Senin, V.; Revazova, E.; A;Title: Isolation and characterization of a gene specifically expressed in different me
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R;Tulchinsky, E.M.; Grigorian, M.S.; Ebralidze, A.K.; Milshina, N.I.; Lukanidin,
Gene 87, 219-223, 1990
A)A:Title: Structure of gene mts1, transcribed in metastatic mouse tumor cells.
A;Reference number: JH0097; MUID:90236313; PMID:2332170
A;Accession: JH0097
A;Molecule type: DNA
A;Residues: 1-101 <TUL>
A;Cross-references: GB:M36578; GB:M36579
B;Experimental source: liver
R;Tulchinsky, B.
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A,Residues: 1-47,'VSGSKFNG',56-57,'RTDEAA' <TUZ>
A,Residues: 1-47,'VSGSKFNG',56-57,'RTDEAA' <TUZ>
A,Cross-references: BMBL:X16094; NID:g53249; PIDN:CAA34224.1; PID:g53250
R,Jackson-Grusby, L.L.; Swiergiel, J.; Linzer, D.I.H.
Nucleic Acids Res. 15, 6677-6690, 1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 DANQDEQUSFKEFUVLUTDVLITAHDNIHKE
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Best Local Similarity 37.4°
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A, Molecule type: mRNA
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1/Molecule type: protein
1/Residues: 1-91 < MAR>
1/Experimental source: adipose tissue
1/Experimental source: adipose tissue
1/Experimental source: N.H.; Inoue, S.; Hidaka, H.
1/Experimental solost in 196, 1995
1/Aitle: S100-beta is a target protein of neurocalcin delta, an abundant isoform in glia
1/Experimen number: S54343; MUID:95194333; PMID:7887910
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).Residues: 56-61,'N',63-79,'V' <OKA>

).Residues: 56-61,'N',63-79,'V' <OKA>

).Comment: The S-100 protein is composed of two related polypeptide chains, alpha and be rain proteins, S-100 is also found in a variety of other tissues.

).Comment: S-100 is an intracellular protein that weakly binds calcium. It binds zinc vere with different affinities exist for both ions on each monomer. Physiological concentry with different affinities exist for both ions on each monomer. Physiological concentry
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                                                                                                                                                                                                                                                                                                                                                                                                     3-100 protein beta chain - bovine

1.Alternate names: neurocalcin delta-binding protein S100-beta
1.Species: Bos primigenius taurus (catle)
1.Date: 31-May-1979 #sequence revision 14-Nov-1983 #text_change 24-Nov-1999
1.Accession: A91254; B91110; A90075; S54348; A03077
1.Accession: A91254; B91110; A90075; S54348; A03077
1. Okuyama, T.

3ur. J. Biochem. 89, 379-388, 1978
1. The amino-acid sequence of S-100 protein (PAP-I-b protein) and its relation to A).Reference number: A91254; MUID:79045265; PMID:710399
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*/Title: Ions binding to $100 proteins: structural changes induced by calcium and zinc 1, 20 contains to $100 proteins: structural changes induced by calcium and zinc 1, 20 contains annotation; metal ion-binding properties

*/Anschak, D.R.; Umekawa, H.; Watterson, D.M.; Hidaka, H.

**Arch. Blochem. Blophys. 240, 777-780, 1985

*/Title: Structural characterization of the calcium binding protein $100 from adipose to $100 from $100 
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,Accession: B91110
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A/Residues: 'ESEL',5-91 <ISO>
A/Experimental source: brain
A/Note: this sequence has since been revised in reference A91110
A/Isobe, T.; Okuyama, T.;
3ur. J. Biochem. 116, 79-86, 1981
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1/Modified site: blocked amino end (Ser) (probably acetylated)
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DANQDEQVSFKEFVVLVTDVLITAHDNIHKE 91
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3; Baudier, J.; Gerard, D.
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S-100 protein alpha chain - bovine
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A;Residues: 1-94 «KUW-
R;Isobe, T.; Okuyama, T.
Bur. J. Biochem. 116, 79-86, 1981
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                                                                                                                                                                                                          nding sites.
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Matches
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A;Title: A growth-related mRNA in cultured mouse cells encodes a placental calcium bindi
A;Reference number: A26803; MUID:87316927; PMID:3628004
A;Accession: A26803
                                                                                                                                                                                 A,Molecule type: mENA
A,Residues: 1-101 <-JAC>
A,Residues: 1-101 <-JAC>
A,Ctrose-references: GBEXO5835, NID:g50310; PIDN:CAA29282.1; PID:g50311
R;Goto, K.; Endo, H.; Fujiyoshi, T.
J. Biochem: 103, 48-53, 1988
A,Fitle: Cloning of the sequences expressed abundantly in established cell lines: identi
A,Reference number: A41411; WUID:88199109; PMID:3162911
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C;Date: 04-Dec-1986 #sequence revision 06-Jan-1995 #text_change 08-Dec-2000
C;Date: 04-Dec-1986 #sequence revision 06-Jan-1995 #text_change 08-Dec-2000
C;Accession: A38364; A92972; A03376
R;Allore, R.J.; Friend, W.C.; O'Markelore, K.M.; Baumal, R.; Dunn, R.J.; Markelore, Chem. 265, 15537-15543, 1990
A;Title: Cloning and expression of the human S100beta gene.
A;Reference number: A38364; MUID:90368757; PMID:2394738
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J. Neurochem. 45, 700-705, 1985
A,Fitle: Characterization of human brain S100 protein fraction: amino acid sequence of SA,Reference number: A92972; MUID:85291729; PMID:4031854
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Biochim. Biophys. Acta 790, 164-173, 1984
A;Title: Purification, characterization and ion binding properties of human brain S100b
A;Reference number: A90653; MUID:85023393; PMID:6487634
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A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-101 <CDT>
A; Residues: 1-101 <CDT
A; Residues: 1-101 <C
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A;Cross-references: EMBL:X16094; NID:g53249; PIDN:CAA34224.1; PID:g53250
C;Comment: Gene mts1 is expressed in metastatic cells.
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N;Alternate names: neural S-100 calcium-binding protein beta
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(Superfamily: S-100 protein, calmodulin repeat homology
C;Keywords: calcium binding; cancer; EF hand
F;7-41/Domain: calmodulin repeat homology <EF1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: I48674; MUID: 93141279; PMID: 8423998
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Best Local Similarity 36.99
Matches 31; Conservative
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A; Residues: 1-92 <ALL>
                                                                                                                                                   .;Status: preliminary
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A; Contents: annotation; metal ion-binding properties C; Comment: This protein binds pas, tubulin and many other proteins at physiological con-C; Comment: S-100 is an intracellular protein that binds calcium. It binds zinc more tigh different affinities exist for both ions on each monomer. Physiological concentrations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANOLE: the first intron occurs before the initiator codon cycles, homodiner; hererodimer with S-100 protein alpha chain (see PIR:BCHUIA) cycuperfamily: S-100 protein; calmodhin repeat homology cycuperfamily: S-100 protein; calmodhin repeat homology cycles hand; heterodimer; homodimer; E;2-92/Product: S-100 protein beta chain #status experimental cMAT> F;6-40/Domain: calmodulin repeat homology cEF1> F;6-40/Domain: calmodulin repeat homology cEF2> F;2/Modified site: blocked amino end (SeX) (in mature form) (probably acetylated) #statu F;19,22,24,27,32/Binding site: calcium (SeX, Glu, Asp, Lys, Glu) #status predicted F;62,64,66,68,73/Binding site: calcium (Asp, Asp, Asp, Glu, Glu) #status predicted
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C.Comment: S-100 is an intracellular protein that weakly binds calcium. It binds zinc vies, with different affinities, exist for both ions on each monomer. Physiological concellicum-binding sites.
                                                                                                                                                                                                          C.Comment: This protein is expressed predominantly in brain tissue by astroglial cells. C.Comment: The homodimer contains disulfide bonds, but the bond pattern has not been de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Bos primigenius taurus (cattle)
C;Abate: 14-Nov-1893 #sequence revision 06-Reb-1995 #text_change 24-Nov-1999
C;Accession: A24156; A91110; $54346; A03078
R;Kuwano, R.; Maeda, T.; Usui, H.; Araki, K.; Yamakuni, T.; Ohshima, Y.; Kurihara, T.;
ERBS Lett. 202, 97-101, 1986
A;Title: Molecular cloning of cDNA of S100alpha subunit mRNA.
A;Reference number: A24156; MUID:86248083; PMID:3755105
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A;Reference number: A91110; MUID:81236562; PMID:7250124
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                                                                                                                                                                                                                                                                                                                                     A;Gene: GDB:S100B
A;Cross-references: GDB:120360; OMIM:176990
A;Map position: 21q22.3-21q22.3
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); Superfamily: S-100 protein; calmodulin repeat homology

Y. Keywords: blocked amino end; brain; calcium binding; EF hand; zinc

1.2-94/Product: S-100 protein alpha chain #sterus predicted <MAT>

1.7-41/Pomain: calmodulin repeat homology <EF1>
1.50-82/Domain: calmodulin repeat homology <EF2>
1.50-82/Domain: calmodulin repeat homology <EF2>
1.50-02/Domain: calmodulin repeat homology <EF2>
1.50-02/Somain: calmodulin calcium (Ser, Glu, Asp, Lys, Glu) #status predicted
1.63,65,67,69,74/Binding site: calcium (Asp, Asn, Asp, Glu, Glu) #status predicted
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33; Indels 0; Gaps Query Match
34.5%; Score 161; DB 1; Length 94;
Best Local Similarity 38.4%; Pred. No. 1.6e-08;
Matches 33; Conservative 20; Mismatches 33; Indels

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1 TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTKDQGTIDKIFQNL 60 SELETAMETLINVFHAHSGKEGDKYKLSKKELKELLGTELSGFLDAQKDADAVDKVMKEL 62

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!earch completed: March 5, 2004, 09:49:26
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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-!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
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R HSSP; P80511; 1E8A.

R InterPro; 1PR001751; CabP_S100.

R InterPro; 1PR002048; EF-hand.

R Pfam; PF01023; S 100; 1.

R ProDom; PD000340; EF-hand; 1.

R ProDom; PD00018; EF-hand; 1.

R PROSITE; PS00018; EF-hand; 1.

R PROSITE; PS00303; S100 CABP; 1.

R Calcium-binding; Zino; Metal-binding.

CA_BIND 61 72 EF-HAND; (LOW AFFINITY) (BY CA_BIND 61 AFF
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B4204461432D7FCE CRC64;
                                                                                                                                                             01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Calgranulin C (CAGC).
                                                                                            91 AA
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Best Local Similarity 100.
Matches 91; Conservative
                                                                                            STANDARD;
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                                                                                   S112 PIG
P80310;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration
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EF-HAND 1 (LOW AFFINITY) (BY SIMILARITY).
EF-HAND 2 (HIGH AFFINITY) (BY
SIMILARITY).
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Cell 97:889-901(1999).
C-1-SIMILARITY: Belongs to the S-100 family.
                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Calgaranulin C (CAGC) (Calcium-binding protein in amniotic fluid 1)
(CAAF1) (RAGE binding protein).
S100A12 OR CAAF1.
Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99325504; PubMed=10399917; Hofmann M.A., Drury S., Fu C., Qu W., Taguchi A., Lu Y., Avila C., Kambann M.A., Drury S., Nawroth P., Neurath M.F., Slattery T., Beach D., McClary J., Nagashima M., Morser J., Stern D., Schmidt A.M.;
                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A novel calcium-binding protein in amniotic fluid, CAAF1: its molecular cloning and tissue distribution."; J. Cell Sci. 109:805-815(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUB-Oesophagua;
MEDLINE-96298783; PubMed=8718672;
Hitomi J., Yamaguchi K., Kikuchi Y., Kimura T., Maruyama K.,
Nagasaki K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 371; DB 1; Length 91;
Pred. No. 7.1e-28;
9; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66FBC3C1B0354482 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P80511; 1EBA.
InterPro; IPR001751; CaBP_S100.
InterPro; IPR001751; CaBP_S100.
InterPro; IPR001751; CaBP_S100.
Pfam; PF00036; efhand; 1.
ProDom; PF0003407; CaBP_S100; 1.
ProDom; PF00012; EF-hand; 1.
PROSITE; PS00018; EF HAND; 1.
PROSITE; PS00303; S100 CABP; 1.
Calcium-binding; Zinc; Metal-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF011757; AAB65423.1; -.
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Best Local Similarity 81.3%;
Matches 74; Conservative 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 AA; 10554 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D49548; BAA08496.1; -.
                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovidae; Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9913;
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                                                       S112 BOVIN
ID S112 BOVIN
AC P79105;
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01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Calgranulin C (CAGC) (CGRP) (Neutrophil S100 protein) (Calcium-binding
protein in amniotic fluid 1) (CAARI) ($6) (Contains: Calcitermin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96192053; PubMed=8619860; Yamamura T., Hitomi O., Nagasaki K., Suzuki M., Takahashi E., Saito S., Tsukada T., Yamaguchi K.; "Human CAAFI gene -- molecular cloning, gene structure, and chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUB=Nasal mucus;
MEDLINE=21413725; PubMed=11522286;
Cole A.M., Kim Y.-H., Tahk S., Hong T., Weis P., Waring A.J., Ganz T.;
"Calcitermin, a novel antimicrobial peptide isolated from human airway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Neutrophils;
MEDLINE=96332419; PubMed=8769108;
MID E.C., Troxler H., Buergisser D.M., Kuster T., Markert M.,
Guignard F., Hunziker P., Birchler N., Heizmann C.W.;
"Amino acid sequence determination of human S100A12 (P6, calgranulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21065388; PubMed=11134923; Moroz O.V., Antson A.A., Murbhudov G.N., Maitland, N.J., Dodson G.G., Wilson K.S., Skibshoj I., Lukanidin E.M., Bronstein I.B.; I.t. tukanidin E.M., Bronstein I.B.; Acta Crystallogr. D 57:20-29(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Marti T., Erttmann K.D., Gallin M.Y., "Host-parasite interaction in human onchocerciasis: identification and sequence analysis of a novel human calgranulin."; Blochem. Blochem. Blochem. 221.454-458(1996).
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97138564; PubMed=8985590; Wicki R., Marchlolz I., Mischke D., Schaefer B.W., Heizmann C.W.; "Characterization of the human S100A12 (calgranulin C, p6, CAAR1, CGRP) gene, a new member of the 8100 gene cluster on chromosome
                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-20.
MEDILINE=95551965; PubMed=7626002;
Guignard F., Mauel J., Markert M.;
Guidnard F., Manal J., Markert M.;
"Identification and characterization of a novel human neutrophil protein related to the $100 family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 77-91, ANTIMICROBIAL ACTIVITY, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem. Biophys. Res. Commun. 221:356-360(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C, CGRP, CAAF1) by tandem mass spectrometry.";
Biochem. Biophys. Res. Commun. 225:146-150(1996)
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              16
                                                                                                                 91
DADKDGAVSFEEFVULVSRVLKTAHIDIHKE
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                                                                                                                               P80511; P83219;
01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell Calcium 20:459-464 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. J. 309:395-401(1995).
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                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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us-09-646-651c-1.rsp

61 DANQDEQVDFQEFISLVAIALKAAHYHTHKE 91

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FUNCTION: Calcitermin possesses antifungal activity against C.albicans and is also active against E.coli and P.aeruginosa but not L.monocytogenes and S.aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CALCITERMIN.
EP-HAND 1 (LOW AFFINITY) (BY SIMILARITY).
EF-HAND 2 (HIGH AFFINITY) (BY
SIMILARITY).
                                                                               MASS SPECTROMETRY: WW=1044; METHOD=Electrospray; RANGE=1-91. MASS SPECTROMETRY: WW=1688.9; METHOD=MALDI; RANGE=77-91. SIMILARITY: Belongs to the $5-100 [amily.] SIMILARITY: Contains 2 EF-hand calcium-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R GO; GO: 0005562; C:cytosol; TAS.
R GO; GO: 0005562; C:insoluble fraction; TAS.
R GO; GO: 0005562; C:insoluble fraction; TAS.
R GO; GO: 0005563; P:alcium ion binding; TAS.
R GO; GO: 00065954; P:inflammatory response; TAS.
R InterPro; IPR001751; CaBP_S100.
R InterPro; IPR003048; BF-hand.
R Pfam; PF00036; efhand; 1.
R Probom; PD000121; BF-hand; 1.
R Probom; PD000121; BF-hand; 1.
R PROSITE; PS000103; S100_CABP; 1.
R PROSITE; PS000303; S100_CABP; 1.
R Calcium-binding; Zinc; Metal-binding; Antibiotic; Fungicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.1%; Score 332; DB 1; Length 91; 70.3%; Pred. No. 2.9e-24; ive 10; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10444 MW; 325685EA8695F6B7 CRC64;
                                                SUBUNIT: Homodimer.
TISSUE SPECIFICITY: Monocytes and lymphocytes.
                                                                                                                                                                                                                                                                                                                                                                        EMBL; X98289; CAB94792.1; -...
EMBL; X98299; CAB94792.1; -...
EMBL; D49549; BAA08497.1; -...
EMBL; D83664; BAA12036.1; -...
EMBL; D83657; BAA12030.1; -...
PIR; JC4712; JC4712.
PDB; IE8A, 08-JAN-01.
PDB; IE8A, 08-JAN-01.
PDB; HGAC.10489; S100A12.
                                                                                                                                                                                                                                                                                                        EMBL; X97859; CAA66453.1; -.
EMBL; X98289; CAA66934.1; -.
EMBL; X98289; CAA66934.1; JOINED.
EMBL; X98290; CAA66934.1; JOINED.
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31
72
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Best Local Similarity
Matches 64; Conserv
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68
70
91 AA;
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77
18
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INIT_MET
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CA BIND
CA BIND
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HELIX
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STRAND
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                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIM-New Zealand white; TISSUE-Neutrophils;
MEDLINE-96355278; PubMed=8702688;
Wang Z., Deveer M.J., Gardiner E.E., Devenish R.J., Handley C.J., Underwood J.R., Robinson H.C.;
"Rabbit polymorphonuclear neutrophils form 35S-labeled S-sulfo-calgranulin C when incubated with inorganic [35S]sulfate.";
J. Biol. Chem. 271:19802-19809(1996)
-: SIMILARITY: Contains 2 EF-hand calcium-binding domains.
                                                                                                                                                Eukaryotā; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64.7%; Score 302; DB 1; Length 81; 70.4%; Pred. No. 1.5e-21; ive 11; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EF-HAND 1 (LOW AFFINITY) (
EF-HAND 2 (HIGH AFFINITY)
SIMILARITY),
95E67A209180CB66 CRC64;
                                            15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Calgranulin C (CAGC) (Fragment).
                 81 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 24, Created)
(Rel. 26, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (St or send an email to license@isb-sib.ch).
                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001751; CaBP_S100.
InterPro; IPR02048; EF-hand.
Pfam; PF00036; efhand; 1.
ProDom; PD003407; CaBP_S100; 1.
ProDom; PD000012; EF-hand; 1.
PROSITE; PS00018; EF-HAND; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 KEFVVLVTDVLITAHDNIHKE 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 KEFLSLLASVLVTAHENIHKE 81
                                                                                                                                  Oryctolagus cuniculus (Rabbit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF091848; AAC61770.1; -
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                 STANDARD;
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NON_TER 1
CA_BIND 8
CA_BIND 51
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01-JUL-1993
               S112 RABIT
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P28783;
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S109 BOVIN
RABIT
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1 TKLEBHLEGIVNIFHQYSVRKGHFDTLSKGELKQLLTKELANTIKNIKDKAVIDBIFGGL 60

61 DANQDEQVSFKEFVVLVTDVLITAHDNIHKE 91

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1 TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTKDQGTIDKIFQNL

64; Conservative

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Query Match
Best Local Similarity
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CA BIND 29
                                                  NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9986;
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P50117;
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                                                                                                                                                                 TISSUE-Desophageal epithelium;
MEDLINE-93280230; PubMed=8505358;
Tang T.K., Hong T.-M., Lin C.-Y., Lai M.-L., Liu C.H.L., Lo H.-J.,
Tang T.K., Gong T.-M., Lin C.-Y., Ip W., Lin D.C., Lin J.J.-C.,
Lin S., Sun T.-T., Wang E., Wang J.L., Wu R., Wu C.-W., Chien S.,
"Nuclear proteins of the bovine esophageal epithelium. I. Monoclonal
antibody W2 specifically reacts with condensed nuclei of
differentiated superficial cells.";
J. Cell Sci. 104:237-247(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Gaps
                                                                                                                                                                                                                                                                                                                                              TISSUE=Neutrophils;
MEDLINE=92304974; PubMed=1610833;
Dianoux A.-C., Stasia M.-J., Garin J., Gagnon J., Vignais P.V.;
"The 23-kilodalton protein, a substrate of protein kinase C, in
bovine neutrophil cytosol is a member of the S100 family.";
Biochemistry 31:5898-5905(1992).
-!- SUBUNIT: Disulfide linked heterodimer of a 7/11 kDa and a 22/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 32 EF-HAND 1 (LOW AFFINITY) (POTENTIAL).
63 74 EF-HAND 2 (HIGH AFFINITY) (POTENTIAL)
122 AA; 13673 WW; F3CA8C48806BECCD CRC64;
                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
15-MAR-2004 (Rel. 43, Last annotation update)
Calgranulin B (Neutrophil cytosolic 23 kDa protein) (P23) (BEB22)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Cytoplasmic; loosely associated to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.4%; Score 263.5; DB 1; Length 122; 53.3%; Pred. No. 8.4e-18; ive 23; Mismatches 18; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Protein MRP-126.
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 LDANQDEQVSFKEFVVLVTDVLITAHDNIH 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001751; CaBP S100.
InterPro; IPR002048; EF-hand.
Pfam; PF000023; efhand; 1.
Pfam; PF01023; S 100; 1.
ProDom; PD000407; CaBP S100; 1.
ProDom; PD000012; EF-hand; 1.
PROSITE; PS000018; EF-hand; 1.
PROSITE; PS00303; S100 CABP; 1.
Calcium-binding; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 53.3%
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                          Bovidae; Bovinae; Bos.
                                                              Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P80511; 1E8A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           kDa subunits.
                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 4-56
                                                                                                                         NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M126_CHICK
ID M126_CHICK
AC P28318;
                                 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                         SEQUENCE
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                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=White leghorn; TISSUB=Bone marrow;
MEDLINE=22195690; PubMed=1549365;
Nakano T., Graf T.,
"Identification of genes differentially expressed in two types of
"Whyb-transformed avian myelomonocytic cells.";
Oncogena 7:227-554 [1922].
-Insura SPECIFICITY: Expressed in v-myb-transformed myelomonocytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTKDQGTIDKIFQNL
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-New Zealand white; TISSUE=Neutrophils;
MEDLINE=96355278; PubMed=8702688;
Yang Z., de Veer M.J., Gardiner E.E., Devenish R.J., Handley C.J., Underwood J.R., Robinson H.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryccolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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16-CCT-2001 (Rel. 40, Last annotation update)
Calgranulin B (Migration inhibitory factor-related protein 14)
(MRP-14) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- SIMILARITY: Belongs to the S-100 family.
-i- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22; Indels
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Pred. No. 8.6e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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HSSP; P04271; 1UWO.
INTERPZO; IPR001751; CaBP_S100.
InterPZO; IPR002048; EF-hand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam, PF00036; efhand; 1.
Pfam, PF01023; S_100; 1.
ProDom; PD003407; CaPP S100; 1.
ProDom; PD000012; EF-hand; 1.
PROSITE; PS00303; SIOO_CABP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42; Conservative
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Miyasaki K.T., Bodeau A.L., Murthy A.R., Lehrer R.I.,
"In vitro antimicrobial activity of the human neutrophil cytosolic S-
100 protein complex, calprotectin, against Capnocytophaga sputigena.";
 SEQUENCE FROM N.A.
MEDLINE=88039099; PubMed=3313057;
Odink K., Cerletti N., Bruggen J., Clerc R.G., Tarcsay L., Zwaldo G.,
Gerhards G., Schlegel R., Sorg C.;
"Two calcium-binding proteins in infiltrate macrophages of rheumatoid
arthritis.";
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-89255276; PubMed-2656677;
Murao S., Collart F.R., Huberman E.;
"A protein containing the cystic fibrosis antigen is an inhibitor of
                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=88302148; PubMed=3405210;
Lagasse E., Clerc R.G.;
Lagasse E., Clerc R.G.;
"Cloning and expression of two human genes encoding calcium-binding proteins that are regulated during myeloid differentiation.";
Mol. Cell. Biol. 8:2402-2410(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Ionomycin-regulated phosphorylation of the myeloid calcium-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E., Vandekerckhove J.;
"Microsequences of 145 proteins recorded in the two-dimensional gel protein database of normal human epidermal keratinocytes.";
Electrophoresis 13:960-969(1992).
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND VARIANT ARG-20.
Wang M., Xu X., Cai Y., Xu H., Han Y., Xu Z., Wu M.;
"Human gene for migration inhibitory factor-related protein
("MPR14), variant allele.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 84-114, AND PHOSPHORYLATION. MEDLINE=90044075; PubMed=2478889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 11-19; 26-37 AND 94-107.
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                                                                                                                                                                                                                                                                                                                                                                   Biol. Chem. 264:8356-8360(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Keratinocytes;
MEDLINE=93162043; PubMed=1286667;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 5-34.
MEDLINE=93139333; PubMed=8423249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein p14.";
Nature 342:189-192(1989)
                                                                                                            Nature 330:80-82(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                    protein kinases."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Lung
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 IINIFHQYSVRLGHYDTLIKRELKQLITKELPNTL-KNTKDQGTIDKIFQNLDANQDEQV 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=New Zealand white;
MEDLINE=94198229; Pubmed=8148323;
Mori S., Goto K., Goto F., Mutakami K., Ohkawara S., Yoshinaga M.;
Morins S., Goto R., Expression of neutrophils during the course of acute inflammation in rabbits.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P06702: Q9NYM0; Q9UGUI)
01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Lagt sequence update)
10-OGT-2003 (Rel. 42, Last annotation update)
Calgranulin B (Migration inhibitory factor-related protein 14)
MRP-14, P14) (Leukocyte L1 complex heavy chain) (S100 calciumbinding protein A9) (Galprotectin L1H subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
"Rabbit polymorphonuclear neutrophils form 35S-labeled S-sulfo-calgranulin C when incubated with inorganic [35S]sulfate."; J. Biol. Chem. 271:19602-19809(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 118;
                                                                                                                                                                           Immunol. 6:149-156(1994).
SIMILARITY: Belongs to the S-100 family.
SIMILARITY: Contains 2 BF-hand calcium-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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51.2%; Pred. No. 1.8e-13;
tive 20; Mismatches 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 SFKEFVVLVTDVLITAHDNIHK 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00036; efhand; 1.
Pfam; PF01023; S_100; 1.
Probom; PD003407; CaBP_S100; 1.
Probom; PD000012; EF-hand; 1.
PROSITE; PS00018; EF HAND; 1.
PROSITE; PS0033; S100 CABP; 1.
NON_TER
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InterPro; IPR001751; CaBP_S100.
InterPro; IPR002048; BF-hand.
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EMBL; D17404; BAA04227.1; -.
PIR; 146861; 146861.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13292 MW;
                                                                       SEQUENCE OF 45-82 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42; Conservative
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118
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118 AA;
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[1]
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Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CA BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Raftery M.J., Gedzy C.L.;
Raftery M.J., Gedzy C.L.;
"Identification of postranslational modifications and cDNA sequencing errors in the rat S100 proteins MRP8 and 14 using electrospray ionization mass spectrometry.";
Anal. Biochem. 258.282-292(1998).
-!- MASS SPECTROMETRY: MM-1369; MW ERR=2; METHOD=Electrospray.
-!- SIMILARITY: Belongs to the $-100 family.
-!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
                                                                                                                                                                                                                                               S100A9 OR MRP14.
Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METHYLATION.

BF-HAND 1 (LOW AFFINITY) (POTENTIAL).

BF-HAND 2 (HIGH AFFINITY) (POTENTIAL).

BF-HAND 2 (RICH AFFINITY)

BF-HAND 381EEB291175D068 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-56; 61-64 AND 71-112, ACETYLATION, AND METHYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECURNCE FROM N.A.
STRAIN=Lewis/N; TISSUE=Peritoneal cavity;
MEDLINE=93343942; PubMed=8943166;
Imamicoli T., Uchida I., Wahl S.M., McCartney-Francis N.;
Imamicoli T., Uchida I., Wahl S.M., McCartney-Francis N.;
Imamicoli T., Uchida I., Wahl S.M., McCartney-Francis N.;
Imprication and cloning of migration inhibitory factor-related protein (MRP)8 and MRP14 in arthritis-susceptible rats.";
Biochem. Biophys. Res. Commun. 194:819-825(1993).
                                                                      01-0CT-1996 (Rel. 34, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
calgranulin B (Migration inhibitory factor-related protein 14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43.8%; Score 204.5; DB 1
41.8%; Pred. No. 2.2e-12;
tive 24; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; JN0686; JN0686; JN0686; JN0686; JN0686; JN0686; JNM6086; JNM6086; JNM6086; JNM6086; JNM601751; CaBP_S100.
InterPro; IPR001751; CaBP_S100.
InterPro; JPR001751; S100; 1.
Propon; PS00018; EF HAND; FALSE_NEG. PROSITE; PS000189; EF HAND; FALSE_NEG. PROSITE; PS000189; EF HAND; FALSE_NEG. PROSITE; PS000303; S100 CABP; 1.
Calcium-binding; Acetylation; Methylation. INTERPROSE 10 10 METHYLATION. MOD_RES 106 EF-HAND 1 (LOW ACET END 23 36 EF-HAND 1 (LOW ACET END 23 36 EF-HAND 1 (LOW ACET END 23 36 EF-HAND 2 (HIGH).
                  112 AA
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                      STANDARD;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
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105
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SEQUENCE
                             S109 RAT
P50116;
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S109 RAT
                                                                  STITITIES NO DE RESERVA DE RESERV
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                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                    FUNCTION: Expressed by macrophages in acutely inflammated tissues FUNCTION: Expressed by macrophages in acutely inflammated tissues and in chronic inflammations. Seem to be an inhibitor of protein kinases. Also expressed in epithelial cells constitutively or induced during dermatoses. May interact with components of the intermediate filaments in moncoytes and epithelial cells. MISCELLANEOUS: Has been shown to bind calcium.

SIMMILARITY: Belongs to the S-100 family.

SIMILARITY: Contains 2 EF-hand calcium-binding domains.
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EF-HAND 2 (HIGH AFFINITY) (POTENTIAL).
PHOSPHORYLATION.
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/FTIG=VAR 013008.

S -> H (IN RAF. 8).

K -> F (IN RAF. 8).

H -> L (IN RAF. 8).

H -> L (IN RAF. 8).
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MIM; 123886; -. GOODSESO; Ficalcium ion binding; TAS.

GO; GO:0005509; Ficalcium ion binding; TAS.

GO; GO:0004712; Fisignal transducer activity; TAS.

GO; GO:0007267; P::ell-cell signaling; TAS.

GO; GO:000554; P::inflammatory response; TAS.

InterPro; IPR001751; CABP_S100.

InterPro; IPR001751; CABP_S100.

InterPro; IPR001751; EF hand; 1.

Pfam; PF00013; S100; 1.

ProDom; PF00018; EF HAND; 1.

PROSITE; PS00018; EF HAND; 1.
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                      J. Dent. Res. 72:517-523(1993)
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CA_BIND 6
MOD RES 11
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50 1 TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTK-DQGTIDKIFQN Gaps 1; 28; Indels 60 LDANQDEQVSFKEFVVLVTDVLITAHDNIHK 90 66 LDTNQDNQLSFEECMALMGKLIFACHEKLHE 96

DB 1; Length 112;

CONFLICT

SEQUENCE

CONFLICT

Query Match

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RESULT 9

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CONFLICT
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Maxs J.L., Wang J., Hsieh F.K.,

Dlatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Dlatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Rapha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunstathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Becker T., Gerke V., Kibbe E., Weber K.; "S100P, a novel Ca(2+)-binding protein from human placenta. CDNA properties."; recombinant protein expression and Ca2+ binding properties."; Fur. J. Blochem. 207:541-547(1992).
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Emoto Y., Kobayashi R., Akatsuka H., Hidaka H.;
"Purification and characterization of a new member of the S-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blochem. Blophys. Res. Comun. 18:1246-1253(1992).
-!- SUBUNIT: Interacts with S1002.
-!- MISCELLANEOUS: This protein binds two calcium ions.
-!- SIMILARITY: Belongs to the S-100 family.
-!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                          01-MAY-1992 (Rel. 22, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
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                                                                                                                             STANDARD;
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SEQUENCE OF 1-91.
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S100P OR S100E.
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EMBL; BC006819; AAH06819.1; PIR; S24146; S24146. PDB; 1J55; 07-JAN-03. Genew; HGNC:10504; S100P.

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2 TELETAMGMIIDVFSRYSGSEGSTQTLTKGELKVLMEKELPGFLQSGKDKDAVDKLLKDL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nacken W.K.F., Lekstrom-Himes J.A., Sorg C., Manitz M.;
"Molecular analysis of the mouse S100A9 gene and evidence that the
myeloid specific transcription factor C/EBPepsilon is not required for
the regulation of the S100A9/A8 gene expression in neutrophils.";
J. Cell. Blochem. 80:606-616(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                   1 TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTKDQGTIDKIFQNL
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96235204; PubMed=8645219; Raftery M.J. Harrison C.A., Alewood P., Jones A., Geczy C.L.; Raftery M.J. Harrison C.A., Alewood P., Jones A., Geczy C.L.; Isolation of the murine S100 protein MRP14 (14 Kpa mylation-linhibitory-factor-related protein) from activated spleen cells: characterization of post-translational modifications and zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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-!- MISCELLANEOUS: Has been shown to bind calcium.
-!- SIMILARITY: Belongs to the S-100 family.
                                                                                                                                                                                                                                                                                                                                   38.8%; Score 181; DB 1; Length 95; 43.3%; Pred. No. 2.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lagasse E., Weissman I.L.;
"Mouse MRP8 and MRP14, two intracellular calcium-binding I associated with the development of the myeloid lineage.";
Blood 79:1907-1915(1992).
                                                                                                                                                                                                                                                                                                                                                                             36; Indels
                                                                                                                                                                                                           EF-HAND 1 (LOW AFFINITY).
EF-HAND 2 (HIGH AFFINITY).
                                                                                                                                                                                                                                                                                           786E6E3F3EACC6C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1993 (Rel. 26, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Calgranulin B (Migration inhibitory factor-related (MRP-14) (P14) (Leukocyte Li complex heavy chain).
                                                                                                                                                                                                                                                   E -> T (IN REF. 3).
F -> E (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                             15; Mismatches
GO; GO:0005509; F:calcium ion binding; TAS.
GO; GO:0005515; F:protein binding; TAS.
InterPro; IPR001751; CaPP_S100.
InterPro; IPR001751; CaPP_S100.
InterPro; IPR001751; CaPP_S100.
Pfam; PF00036; efhand; 1.
ProDom; PD003407; CaBP_S100; 1.
PROSITE; PS00018; EF HĀND; FALSE_NEG.
PROSITE; PS00018; EF HĀND; FALSE_NEG.
CA_BIND
19 32 BF-HAND I (LOW.
CA_BIND
19 32 BF-HAND I (LOW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DANQDEQVSFKEFVVLVTDVLITAHDNIHK 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DANGDAQVDFSEFIVFVAAITSACHKYFEK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=129/SvJ;
MEDLINE=21102096; PubMed=11169745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-9; 75-92 AND 94-108.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=BALB/c;
MEDLINE=92223366; PubMed=1373330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. 316:285-293(1996).
                                                                                                                                                                                                                                                                                         10400 MW;
                                                                                                                                                                                                                                                                                                                                                      Local Similarity 43.3%
les 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Mouse)
                                                                                                                                                                                                                            62
32
44
95 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S109 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  binding.";
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MEDLINE=91359841; PubMed=1653388;
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                                                                                                                                                                                                                               Pfam; PF01023; S_100; 1.
ProDom; PD003407; CabP S100; 1.
ProDom; PD000012; EF-Hand; 1.
PROSITE; PS00018; EF SAND; 1.
PROSITE; PS00303; S100_CABP; 1.
                                                                                                                                                                              InterPro; IPR001751; CaBP S100.
InterPro; IPR002048; EF-hand.
                                                                                                                                                                                                                                                                                                                                                                         92 AA; 10021 MW;
                                                                                                                                          EMBL; U33273; AAB52610.1; -. HSSP; P30801; 1A03.
                                                                                                                                                                                                              Pfam; PF00036; efhand; 1.
Pfam; PF01023; S 100; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                          32
                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                       Calcium-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                             34;
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CA_BIND
SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKONTK-DQGTIDKIFQN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 SQMERSITTIDIFFHQYSRKBGHPDTLSKKEFRQMVBAQLATFWKKEKRNBALINDIMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular cloning of ictacalcin: a novel calcium-binding protein from the channel catfish, Ictalurus punctatus.";

Brain Res. Mol. Brain Res. 41:81-89(1996).
-!- FUNCTION: Plays an important role in catfish calcium homeostasis.
-!- TISSUE SPECIFICITY: Abundant in epithelial cells of olfactory rosette, barbel, skin and gill but not brain or muscle.
-!- SIMILARITY: Belongs to the S-100 family.
-!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
Ictaluridae; Ictalurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                        BF-HAND 1 (LOW AFFINITY) (POTENTIAL). BF-HAND 2 (HIGH AFFINITY) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38.2%; Score 178.5; DB 1; Length 112; 36.3%; Pred. No. 5.6e-10; ive 27; Mismatches 30; Indels 1
-!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Clfactory epithelium;
BDLINES-19138343; PubMed=8883937;
Porta A.R., Bettini E., Buiakova O.I., Baker H., Danho W.,
Margolis F.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METHYLATION.
A0F810BC175AEC80 CRC64;
                                                                                                                                                                   EMBL; M83219; AAB07228.1; --
EMBL; AJ250466; CAC14292.1; --
FIR, S68242; S68242.
HSSP; R6811; LEBA.
MGD; MGI:1338947; S100a9.
InterPro; IPR001751; CaBP_S100.
InterPro; IPR001751; CaBP_S100.
FroDom; PF01023; S100, 1.
ProDom; PD003407; CaBP_S100; 1.
ProDom; PS00012; BF-hand; 1.
PROSITE; PS00012; BF-hand; 1.
PROSITE; PS00013; SIOO_CABP; 1.
CACICIUM-binding; Acetylation; Methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Ictacalcin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 LDANODEOVSFKEFVVLVTDVLITAHDNIHK 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACETYLATION,
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12918 MW;
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Matches 33; Conservative
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CA BIND
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MOD_RES
SEQUENCE
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QY Db 8 8

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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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Ohtsuka E., Ikehara M., Takahashi Y.;
"Molecular cloning and nucleotide sequences of CDNA and genomic DNA
for alpha and beta subunits of S100 protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EF-HAND 1 (LOW AFFINITY) (POTENTIAL).
EF-HAND 2 (HIGH AFFINITY) (POTENTIAL)
DBFE786B7F921C58 CRC64;
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Brain Res. Mol. Brain Res. 10:193-202(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.5%; Score 166; DB 1; Length 92; 41.5%; Pred. No. 6.5e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tanaguchi Symp. Brain Sci. 19:243-255(1987).
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13-AUG-1987 (Rel. 05, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
$10.00 protein, beta chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.5%; Preq. mc.
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91 AA;
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                                                                                                                                                                                                                                                           18
61
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72
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73
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87
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HELIX
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S10Z HUMAN
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TURN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96387197; PubMed=8794737; Drohat A.C., Amburgey J.C., Abildgaard F., Starich M.R., Baldisseri D.M., Weber D.J.; Solution structure of rat apo-51008(beta beta) as determined by NMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99226808; PubMed=10211826; Drohat A.C., Tjandra N., Baldisseri D.M., Weber D.J.; Tjandra N., Baldisseri D.M., Weber D.J.; The use of dipolar couplings for determining the solution structure
                                        Reduction in S100 protein beta subunit mRNA in C6 rat glioma cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P:induction of apoptosis; ISS.
P:learning and/or memory; ISS.
P:positive regulation of complement activation; ISS.
Dunn R., Landry C., O'Hanlon D., Dunn J., Allore R., Brown I.,
                                                                                                                                                                                                                                                                                                                             Drohat A.C., Baldisseri D.M., Rustandi R.R., Weber D.J.; "Solution structure of calcium-bound rat S100B(betabeta) as determined by nuclear magnetic resonance spectroscopy.";
                                                             following treatment with anti-microtubular drugs.";
J. Biol. Chem. 262:3562-3566(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G0:0005509; F:calcium ion binding; ISS.
G0:0019210; F:kinase inhibitor activity; ISS.
G0:004156; F:tau protein binding; ISS.
G0:0008270; F:tau protein binding; ISS.
G0:00048143; P:astrocyte activation; ISS.
G0:00046143; P:astrocyte activation; ISS.
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GO:0006112; P:energy reserve metabolism; ISS.
GO:0048151; P:hyperphosphorylation; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M54919; ARA42096.1; --
EMBL; M55327; -; NOT_ANNOTATED_CDS.
EMBL; M55327; -; NOT_ANNOTATED_CDS.
EMBL; M15705; -; NOT_ANNOTATED_CDS.
EMBL; M15705; -; NOT_ANNOTATED_CDS.
PDB; 1QLK; 11-NOV-98.
PDB; 1DT7; & C-UTL-00.
PDB; 1DT7; & C-UTL-00.
PDB; 1DT7; & C-UTL-00.
PDB; 1DT7; & C-UTL-00.
PDB; IMWN; 18-DEC-02.
GO; GO:0005737; C:CYTOPLASM; ISS.
GO; GO:0005737; C:CYTOPLASM; ISS.
GO; GO:0005509; F:Calcium ion binding
GO; GO:0005509; F:Calcium ion binding
GO; GO:0005709; F:Calcium ion binding
GO; GO:0005709; F:Calcium ion binding
GO; GO:0008270; F:Zinc ion binding
GO; GO:00084143; P:astrocyte activatio
GO; GO:0006414; P:calcium ion homeost
GO; GO:0006412; P:Penergy reserve meta
GO; GO:0006412; P:Penergy reserve meta
GO; GO:0006814; P:Penergy reserve meta
GO; GO:0006814; P:Penergy reserve meta
GO; GO:0006817; P:Penergy reserve meta
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GO:0005576; C:extracellular; ISS.
                                                                                                                                                                                                                                                                                       STRUCTURE BY NMR.
MEDLINE=98153156; PubMed=9485423;
                                                                                                                                                                                                                              spectroscopy.";
Biochemistry 35:11577-11588(1996)
                                                                                                                                                                                                                                                                                                                                                                                              Biochemistry 37:2729-2740(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rat apo-S100B.";
                                                                                                                          STRUCTURE BY NMR
                     Marks A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gribenko A.V., Hopper J.E., Makhatadze G.I.; "Molecular characterization and tissue distribution of a novel member of the S100 family of EF-hand proteins."; Biochemistry 40:15538-15548(2001).
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                   long-term neuronal synaptic p. protein biosynthesis; ISS.
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                   cytokine biosynthesis; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35.1%; Score 164; DB 1; Length 91; 37.4%; Pred. No. 9.8e-09; tive 19; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
GO; GO:0042035; P:regulation of cytokine biosynthesis; GO; GO:0048169; P:regulation of long-term neuronal syn GO; GO:0006417; P:regulation of long-term neuronal syn InterPro; IPR001751; CaBP_S100.

R Ffam; PF00036; efhand; 1.

PFam; PF01023; S100; 1.

PROSITE; PS00018; EF HĀND; 1.

PROSITE; PS003407; CaBP_S100; 1.

RPOSITE; PS00303; S100 CABP; 1.

Calcium-binding; Zinc; Metal-binding; 3D-structure.

O 0 0 EF-HAND 1 (LOW AFFINITY).

CA_BIND 61 72 EF-HAND 2 (HIGH AFFINITY).

HELIX 2 17
                                                                                                                                                                                                                                                                                                                                                                                                     (LOW AFFINITY). (HIGH AFFINITY)
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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MEDLINE=22388257; PubMed=12477932;
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SEQUENCE FROM N.A.
       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
1 TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTKDQGTIDKIFQNL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P27055; P31724;
01-AUG-1992 (Rel. 23, Created)
01-NUV-1995 (Rel. 23, Last sequence update)
15-OCT-2001 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Calgranulin A (Migration inhibitory factor-related protein 8) (MRP-8)
(R8) (Lukkocyte L1 complex light chain) (Chemotactic cytokine CP-10)
(Pro-inflammatory S100 cytokine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                        -!- MISCELLANEOUS: This protein binds two calcium ions.
-!- SIMILARITY: Belongs to the S-100 family.
-!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                  35.1%; Score 164; DB 1; Length 98; 41.9%; Pred. No. 1.1e-08; Live 17; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                             19 32 BF-HAND 1 (LOW AFFINITY).
62 73 BF-HAND 2 (HIGH AFFINITY).
98 AA; 11430 MW; A2053E1809E0F401 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 DANQDEQUSFKEFVVLVTDVLITAHD 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 DANKDNEVDFNEFVVMVAALTVACND 87
                                                                                                                                                                                                                                                                                                               Pfam, PF00036; efhand; 1.
Pfam, PF01023; S_100; 1.
ProDom; PD003407; CaBP S100; 1.
ProDom; PD000118; EF-hand; 1.
PROSITE; PS00018; EF HAND; 1.
PROSITE; PS00303; S100_CABP; 1.
                                                                                                                                                                                                                                                                          EMBL, AF437876, AAL30893.1; -.
BMBL, BOC2320, AAH2320.1; -.
INTERPIC, IPR001751; Cabp. S100.
InterProj. IPR002048; EF-hand.
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 41.9*
Matches 36; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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X MEDLINE=9218405; PubMed=155987;

Lackmann M., Cornish C.J., Simpson R.J., Moritz R.L., Geczy C.L.;

Lackmann M., Cornish C.J., Simpson R.J., Moritz R.L., Geczy C.L.;

Lackmann M., Cornish C.J., Simpson R.J., Moritz R.L., Geczy C.L.;

T "Purification and structural analysis of a murine chemotactic

Cytokine (CP-10) with sequence homology to S100 proteins.";

J. Biol. Chem. 267:7489-7504 (1992).

J. SUMILARITY: Homodimer and/or heterodimer.

J. MISCELLANBOUS: Binds two calcium ions per molecule with an affinity similar to that of the S-100 proteins (By similarity).

J. SIMILARITY: Contains 2 EF-hand calcium-binding domains.
                                                                                                                                                                                                                                                                                              Lackmann M., Rajasekariah P., Iismaa S.E., Jones G., Cornish C.J., Hu S., Simpson R.J., Moritz R.L., Geczy C.L.; "Identification of a chemotactic domain of the pro-inflammatory S100 protein CP-10.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRUBLINGER: STRAINS-129/SvJ; TISSUBLINGER: STRAINS-129/SvJ; TISSUBLINGE-8611640; MEDLINE-96190772; PubMed-8611640; Nacken W.K.F., Manitz M.P., Sorg C.; "Molecular characterisation of the genomic locus of the mouse MRP8
                              Lagasse E., Weissman I.L.; "Mouse MRP8 and MRP14, two intracellular calcium-binding proteins associated with the development of the myeloid lineage.";
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EF-HAND 2 (HIGH AFFINITY) (POTENTIAL
E -> D (IN REF. 3).
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Biochim. Biophys. Acta 1315:1-5(1996)
MEDLINE=92223366; PubMed=1373330;
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Pfam; PF01023; S 100; 1.
ProDom; PD003407; CaBP 5100; 1.
PROSITE; PS00018; EF HAND; 1.
Calcium-binding; Chemotaxis.
INIT MET
CA_BIND
19
32 EF-H4
                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunol. 150:2981-2991(1993).
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InterPro; IPR001751; CaBP_S100.
InterPro; IPR002048; EF-hand.
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                                                                                                                                                 Blood 79:1907-1915(1992).
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1 TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTKDQGTIDKIFQNL 60

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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. [1]

(Mouse)

Mus musculus

2 SELEKALSNLIDVYHNYSNIQGNHHALYKNDFKKMVTTECPQFVQNI----NIENLFREL 57

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compu	ein - protein search, using sw model	March 5, 2004, 09:43:08 ; Se. (w	US-09-646-651C-1 score: 467 e: 1 TKLEDHLEGIINIFHQYSVR	table: BLOSUM62 Gapop 10.0 , Gapext 0.5	d: 1017041 seqs, 315518202 residues	number of hits satisfying chosen parameters	DB seq length: 0 DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	<pre>1:</pre>	1. No. is the number of results re greater than or equal to the is derived by analysis of the t	SUMMARIES Ouery Score Match Length DB ID	289 61.9 70 6 09TR16 193 41.3 100 13 072VA4 178 38.1 99 11 093395 167 35.8 92 11 0925T3 164 35.1 92 11 095KF6 163 34.9 94 11 09D3M4 163 34.9 94 11 09D3M4 164 33.0 2496 11 09LV7 154 33.0 2496 11 09KHD8 151 32.3 69T 4 01720 151 32.3 69T 4 09H4U2 148 31.7 101 6 09TV6 148 31.5 1218 4 095331 145 31.0 213 4 09H4U1
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RESULT OF STANDARD

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1 TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELFNTLKOTKDQSTIDKIFQNL 60

6 S

61 DANQDEQVSF 70 ||::||| 61 DADKKGAVVF 70

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Query Match 61.9%; Score 289; DB 6; Length 70; Best Local Similarity 81.4%; Pred. No. 3.3e-20; Matches 57; Conservative 6; Mismatches 7; Indels

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Matches 35; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. Wang C., Callard G.V.; Wang C., Callard G.V.; "Molecular cloning and stage dependence of an S-10 cDNA from the shark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 LEDHLEGIINIFHQYSVRLGHYDTLIKKELKQLITKELPNTLKNTKDQGTIDKIFQNLDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Danio rerio).
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Squalus acanthias (Spiny dogfish).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Chondrichthyes,
Elasmobranchii; Squalea, Squaloidei; Squalidae; Squalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           41.3%; Score 193; DB 13; Length 100;
46.1%; Pred. No. 6.3e-11;
ive 17; Mismatches 31; Indels
                                                                                                                                                                                                                                         Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
R Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
R EMBL; BC045541; AAH45941.1; -.
R GO, 6005509; F:calcium ion binding; IEA.
RINEAPRO; IPR00171; CaBP S100.
R InterPro; IPR002048; EF-hand.
R Ffam; PF001023; S100; 1.
R Fram; PF01023; S100; 1.
R FAMD; SMART; SM00054; EF, 100; 1.
R RAMET; SM00054; EF, 11.
DR ROSITE; PS00108; EF HAND; 1.
DR ROSITE; PS00108; SE HAND; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF421551; AAN63527.1; -.
EMBL; AF421551; AAN63527.1; -.
EC; GO: GOO5509; F: calcium ion binding; IEA.
InterPro; IPR001751; CaBP_S100.
InterPro; IPR002048; EF-hand.
Pfam; PF00036; efhand; 1.
Pfam; PF01023; S.100; 1.
ProDom; PD003407; CaBP_S100; 1.
ProDom; PD003407; CaBP_S100; 1.
SMART; SM00054; EFh; 1.
                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
SEQUENCE 100 AA; 11157 MW; DAB81814E54CB8C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
S-100 calcium-binding protein Al.
                                                      100 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91
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                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 Similarity 46.1%;
41; Conservative 1
                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                   SEQUENCE FROM N.A. TISSUE=Body;
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                                                Q7ZVA4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                       RESULT 2
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                                     7 ZVA4
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                                                                                                                                                              1 TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTKDQGTIDKIFQNL
                                                                                                                                                                                             2 TELESAMAGIIGVFRKYSGKEGDKYSLSNNEMVDLLKAELPNFIKSQKDKAAVDKIMKDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 SQLESSMESLITVFHRYADKDGDCNTLSKKELKELMQTELASFLKSQKDPAAIDTIMKDL
                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salvelinus fontinalis (Brook trout) (Brook char).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei,
Protacanthopterygii; Salmoniformes; Salmonidae, Salvelinus.
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                                                                                       Length 99;
                                                                                                                          31; Indels
PS00018; EF HAND; 1.
PS00303; SIGO CABP; 1.
99 AA; 11050 MW; BA62D8190A4A3693 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11285 MW; BF45582FF9279D0A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
$100-like calcium binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.1%; Score 178; DB 13;
45.1%; Pred; No. 1.7e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
                                                                                 38.1%; Score 178; DB 13; 40.7%; Pred. No. 1.7e-09; tive 20; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OVAIY,";
Gene 257:187-194(2000).
--- SIMILARITY: BELONGS TO THE S-100 FAMILY
EMBL; AF077613; AAC28367.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO, GO:0005509; F:calcium ion binding; IEA.
InterPro; IPR001751; CaBP S100.
InterPro; IPR002048; EF-hand.
Pfam; PF01023; G-fland; 1.
                                                                                                                                                                                                                                             61 DANQDEQVSFKEFVVLVTDVLITAHD 86
                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 DANODEQUSFKEFUVLVTDVLI 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DONGDGKVSFEEFVSLVVGLSI 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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Probom, PD0004017; CabP S100; 1.
PROSITE; PS00018; EF-hand; 1.
PROSITE; PS00018; EF-hAND; 1.
PROSITE; PS00303; S100 CABP; 1.
SEQUENCE 101 Ab. 1177.
                                                                                                                        35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 45.1.
These 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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XA Azawa J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Azawa J., Shinagawa A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Azawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburac M., Batalov S., Casavant T., Saito R., Kadota K., Matsuda H.A., Ashburac M., Batalov S., Casavant T., Sa Kadota K., Matsuda H.A., Shaburac M., Batalov S., Casavant T., Sakani L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Daska K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Burnstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Sakamoto N., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Hasegawa Y., Kawaji H., Kohtsuki S.,
                       MEDLINE=94376615; PubMed=8090068;
Bettini B., Porta A.R., Dahmen N., Wang H., Margolis F.L.;
"Expressed sequence tags (EST) identify genes preferentially expressed in carfish chemosensory tissues.";
Brain Res. Mol. Brain Res. 23:285-291(1994).
-! SIMILARITY: BELONGS TO THE S-100 FAMILY.
HSSP; PS0801; HAG.
GO; GO:0005509; F:calcium ion binding; IEA.
InterPro; IPR001751; CaBP S100.
InterPro; IPR002048; EF-hand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 IINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTKDQGTIDKIFQNLDANQDEQVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S100A1.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalía; Eutheria; Rodentía; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                  Pfam, PF00036; efhand; 1.
Pfam, PF01023; S_100; 1.
ProDom; PD00012; S=Pand; 1.
PrOSITE; PS00018; EF-hand; 1.
PROSITE; PS00018; EF-hand; 1.
PROSITE; PS00303; S100 CABP; 1.
SRQUENCE 92 AA; 10022 MW; E04875D0C9921C50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.1%; Score 164; DB 13;
41.5%; Pred. No. 3.2e-08;
tive 15; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 17, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J; TISSUB=Head;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 FKEFVVLVTDVLITAHDNIHKE 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S100 calcium binding protein Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9D3M4;
01-JUN-2001
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                                                                                                                                                                                                                                                            Kuge O., Yamakawa Y., Nishijima M.;
"Enhancement of transport-dependent decarboxylation of
phosphatidylserine by S100B protein in permeabilized Chinese hamster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                Cricetulus griseus (Chinese hamster).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35.8%; Score 167; DB 11; Length 92; 38.5%; Pred. No. 1.7e-08; Live 19; Mismatches 37; Indels
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
S100B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY'2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 DANQDEQVSFKEFVVLVTDVLITAHDNIHKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35, Conservative
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                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                NCBI_TaxID=10029;
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Matches

ESULT 6 19PSF6

Nature 409:685-690(2001).
-!- SIMILARITY: BELONGS TO THE S-100 FAMILY.
BMBL, AK017279; BAB30670.1; -.
MGD; MG1:1338917; \$100a1.
GO; GO:0005509; F:calcium ion binding; IEA.

Eukaryota, Metazaa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Siluriformes, Ictaluridae, Ictalurus.

SEQUENCE FROM N.A. NCBI\_TaxID=7998;

0

Gaps

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Length 92; 33; Indels

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Q9JL08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adachi J. Alzawa K., Akahira S., Akimura T., Aono H., Arai A.,
Adachi J., Alzawa K., Akahira S., Akimura T., Aono H., Arai A.,
Adachi J., Alzawa K., Akahira S., Ruunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kato H., Kawai J., Kojima Y.,
Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A.,
Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A.,
Konno H., Saito H., Saito R., Sakai K., Ohno M., Okazaki Y., Okido T.,
Owa C., Saito H., Saito R., Shinagawa A., Shiraki T., Sogabe Y.,
Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y.,
Toya T., Yamamura T., Yasunishi A., Yoshino M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUB=Kidney;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
                                                                                                                                                                                                                                                                   1 TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTKDQGTIDKIFQNL
                                                                                                                                                                                                                                                                                          SELESAMETLINVFHAHSGKEGDKYKLSKKELKDLLQTELSGFLDVQKDADAVDKVIKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
11 days embryo cDNA, RIKEM full-length enriched library,
clone:2700088D09, full insert sequence (S100 calcium binding protein
Al) (Adult male kidney cDNA, RIKEN full-length enriched library,
clone:0610031F03, full insert sequence).
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIKEN FANTOM Consortium.; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                ٥;
                                                                                                                                                                                           DB 11; Length 94;
                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                    7C8E817D135C2D15 CRC64;
                                                                                                                                                                                                                                34;
                                                                                                                                                                                         Query Match 34.9%; Score 163; DB 11;
Best Local Similarity 39.5%; Pred. No. 4.1e-08;
Matches 34; Conservative 18; Mismatches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-C57BL/6J; TISSUE-Kidney;
MEDLINE=99279253; PubMed=10349636;
Carninoi P., Hayashizaki Y.,
Hayashizaki Yi,
Hayashizaki Yi,
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 AA.
                                                                                                                                                                                                                                                                                                                                            DANQDEQVSFKEFVVLVTDVLITAHD 86
                                                                                                                                                                                                                                                                                                                                                                 | | | : | | | | : | | | | | DENGDGEVDFKEYVVLVAALTVACNN 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6J; TISSUE=Kidney;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                Pfam; PF00036; efhand; 1.
Pfam; PF01023; S_100; 1.
ProDom; PD003407; CaBP_S100; 1.
ProDom; PD000012; EF-hand; 1.
PROSITE; PS00018; EF_HAND; 1.
PROSITE; PS00303; S100 CABP; 1.
SEQUENCE 94 AA; 10487 MW; 7C81
InterPro; IPR001751; CaBP_S100.
InterPro; IPR002048; EF-hand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 409:685-690(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S100A1.
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1 TKLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTKDQGTIDKIFQNL 60
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Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SELESAMETLINVFHAHSGKEGDKYKLSKKELKDLLQTELSGFLDVQKDADAVDKVMKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                     STRAIN=C57BL/60; TISSUE-Kidney;
STRAIN=C57BL/60; TISSUE-Kidney;
STRAIN=C57BL/60; TISSUE-Kidney;
Stibata K., Itch M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itch M., Aizawa K., Kusuai T., Tashiro H., Itch M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Tozawa M., Ohara E., Watshiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Otara E., Watshiki M., Riffe integrated sequence analysis (RISA) system-384-format Sequencing pipeline with 384 multicapillary sequencer.";
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Du X.-J., Cole T.J., Tenis N., Gao X.-M., Kontgen F., Kemp B.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7C8E817BBF36ED15 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.9%; Score 163; DB 11; 39.5%; Pred. No. 4.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 $100 calcium binding protein Al (Fragment).
$100A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DANQDEQVSFKEFVVLVTDVLITAHD 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01023; S 100; 1.
ProDom; PD003407; CaBP_S100; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probom; rboolly; EF-hand; 1.
Probom; PS00012; EF-hand; 1.
PROSITE; PS0013; EF HAND; 1.
PROSITE; PS00303; SIOO CABP; 1
SPOTTRNCE 94 AA; 10505 MW;
                                                                               Genome Res. 10:1617-1630(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00036; efhand; 1.
Pfam; PF01023; S_100; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=129/Sv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                               SEQUENCE FROM N.A.
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2 KLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTKDQGTIDKIFQNLD
                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21601613; PubMed=11572870;
                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HORNERIN OR 1110033K19RIK.
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                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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Best Local Similarity
Matches 30; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=ICR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hornerin.
                                                                                                                                                                                                                                                                                                                                                                                                      овунов;
                                                                                                                                                                                                                                                                                                                                                                          OBVHD8
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                                                                                                                                                                                                                                                                                                                                                                                                      DDT SEARCH DESCRIPTION OF SEARCH DESCRIPTION
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STRAIN=C57BL/6J; TISSUE=Aorta, and Vein;

MEDLINE=22354683; PubMed=1246681;

A The FANTOM Consortium.

A the RAKEN Genome Exploration Research Group Phase I & II Team;

A halysis of the mouse transcriptome based on functional annotation of

F 60,770 full-length oDNAs.";

I Mature 420:563-571(2002)

R MBL; AK041026; BAC30787.1; -.

R GO; GO:0005509; F:calcium ion binding; IEA.

R InterPro; IPR001751; CaBP S100.

R InterPro; IPR001751; CaBP S100.

R InterPro; IPR002048; EF-hand.

R Pfam; PF01023; S_100; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 SELESAMETLINVFHAHSAQEGDKYKLSKKELKDLLQTELSGFLDVQKDADAVDKVMKEL 62
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                       Kiewitz R., Lyons G.E., Schafer B.W., Heizmann C.W.; "Transcriptional regulation of S100Al and expression during mouse heart development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 34.7%; Score 162; DB 11; Length 79; Best Local Similarity 44.2%; Pred. No. 4.3e-08; Matches 34; Conservative 14; Mismatches 29; Indels
                                                                                                                                                           Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE S-100 FAMILY.
HENBL; AF218351; AAF32320.1; -.
HSSP; DA6631; 1BAC.
MGD; MGI:1338917; S100a1.
MGD; MGI:005509; F:calcium ion binding; IEA.
InterPro; IPR002048; EF-hand.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Weakly similar to DJ14N1.2 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00036; efhand; 1.
Pfam; PF01023; S 100; 1.
ProDom; PD000012; CaBP 5100; 1.
PROSITE; PS00018; EF HAND; 1.
PROSITE; PS00018; EF HAND; 1.
PROSITE; PS0303; S100-CABP; 1.
NON TER, 79 79 79 SEQÜENCE 79 AA; 8863 MW; F94E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01023; S_100; 1.
ProDom; PD003407; CaBP_S100; 1.
ProDom; PD000012; EF-hand; 1.
PROSITE; PS00018; EF HAND; 1.
PROSITE; PS00303; SIŌO_CABP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 DENGDGEVDFKEYVVLV 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OBBLX1;
01-MAR-2003 (TrEMBLrel, 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 DANQDEQVSFKEFVVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESULT 10
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0;

Gaps

0

30; Conservative

Matches

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o;
                                       62
61
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                        3 KLLESIVIVIDVEYOYATEYGNCDMLSKEBMKELLVTEFHOILKNPDDPDTVDIIMONLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 KLLESIVTVIDVFYQYATEYGNCDMLSKEEMKELLVTEFHQILKNPDDPDTVDIIMQNLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KLEDHLEGIINIFHQYSVRLGHYDTLIKRELKQLITKELPNTLKNTKDQGTIDKIFQNLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Makino T., Takaishi M., Morohashi M., Huh N.-H.;
"Hornerin, a Novel Profilaggrin-like Protein and Differentiation-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pfam; PF01023; S 100; 1.
ProDom; PB003407; CaBP S100; 1.
PROSITE; PS00018; PE HAND; 1.
PROSITE; PS00303; S100 CABP; 1.
SEQUENCE 2496 AA; 247588 MW; 4CE136CA6CE657DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.0%; Score 154; DB 11;
33.3%; Pred. No. 1.1e-05;
tive 23; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        specific Marker Isolated from Mouse Skin.";
J. Biol. Chem. 276:47445-47452 (2001).
-- SIMILARITY: BELONGS TO THE S-100 FAMILY.
EMBL; AY027660; AAKIS791.1; --
                                                                                                                                                                                                                                        2496 AA
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                                                                                    91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:1915973; Hornerin.
GO; GO:0001533; C:cornified envelope; IDA.
InterPro; IPR001751; CBP_S100.
InterPro; IPR002048; EF-hand.
                                                                                                              62 ANQDEQVSFKEFVVLVTDVLITAHDNIHKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 ANODEQVSFKEFVVLVTDVLITAHDNIHKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIŜSUE-PLACENTA;
MEDLINE-93054736; PubMed=1429717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Metastasin.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 LLENIFALINLFKOYSKKDKNTDTLSKKELKELLEKEFRQILKNPDPPDMVDVFMDHLDI 63
                                                    Presland R.B., Haydock P.V., Fleckman P., Nirunsuksiri W., Dale B.A., "Characterization of the human epidermal profilaggrin gene. Genomic organization and identification of an S-100-like calcium binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                          PROTECLYTICALLY CLEAVED.
POLYMORPHISM: A NUMBER OF PROFILAGGRIN ISOFORMS HAVE BEEN FOR WHICH DIFFER BOTH IN SEQUENCE AND IN THE NUMBER OF FILAGGRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35; Indels
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R PIR; A45118; A45118.

R HSSP; R45118; A45118.

R HSSP; R45119; A45118.

R HSSP; R6118; A45118.

R HSSP; R6118; A55118.

R GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0005509; F:calcium ion binding; IEA.

R GO; GO:0005509; F:calcium ion binding; IEA.

R GO; GO:0005509; F:calcium ion binding; IEA.

R GO; GO:0005198; F:structural molecule activity; IEA.

R INTERPORT SPR00145; F:laggrin.

R Pfam; PF01023; F:laggrin; 2.

R Pfam; PF01023; S:lo0; 1.

R PROSITE; PS00018; BF HAND; 1.

R PROSITE; PS00303; SIOO.CABP; 1.

PROPEP.

R PROPER.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILAGGRIN.
SITE I (BY SIMILARITY).
SITE II (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.3%; Score 151; DB 4;
34.8%; Pred. No. 4.2e-06;
tive 23; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   end) (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 NODEQVSFKEFVVLVTDVLITAHDNIHKE 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 DHNKKIDFTEFLLMVFKLAQAYYESTRKE 92
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POTENTIAL.
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                                                                                                                                                                                                                                                                                                                               EMBL; L01089; AAA60177.1; -. EMBL; L01090; AAA60176.1; -.
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01-MAR-2001 (TEMBLEEL 16,
01-OCT-2003 (TEMBLEEL 25,
DJ14N1.1.1 (Profilaggrin 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 34.8% Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               467
474
>591
32
73
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Homo sapiens (Human)
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19
62
591
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                                                                                                                                                                                                                                                                                                              REPEATS
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SEQUENCE
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CHAIN
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Q9H4U2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
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Miyamori H., Hasegawa K., Kim K., Sato H.;
Miyamori H., Hasegawa K., Kim K., Sato H.;
"Expression of metastrasis associated mts1 gene is co-induced with membrane type-1 matrix metalloproteinase (MT1-MMP) during oncogenic transformation and tubular formation of madin darby canine kidney (MDCK) epithelial cells.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
-: SIMILARITY: BELONGS TO THE S-100 FAMILY.
EMBL; AB031064; BA83419-1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Canis familiaris (Dog).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.3%; Score 151; DB 4; Length 687; 34.8%; Pred. No. 5e-06; ive 23; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31.7%; Score 140; DB 6; Length 101; 34.5%; Pred. No. 1.2e-06; itve 23; Mismatches 32; Undels
                                                                                              Host, Golouls, Inch.

GO; GO:0005198; F:calcium ion binding; IEA.

GO; GO:0005198; F:carctural molecule activity; IEA.

Interpro; IPR001751; GaBP 5100.

Interpro; IPR002048; EF-hand.

Interpro; IPR003303; Filaggrin.

Fram; PF00316; efhand; 1.

Fram; PF03516; Filaggrin; 3.

Fram; PF03516; Filaggrin; 3.

PFNNTS; PR0487; FILAGGRIN.

PROSITE; PS00018; EF HAND; 1.

PROSITE; PS00018; EF HAND; 1.

PROSITE; PS00018; EF HAND; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              76659 MW; 8000363FBEF07B74 CRC64;
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Last annotation update)
-!- SIMILARITY: BELONGS TO THE S-100 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0005509; F:calcium ion binding; IEA.
InterPro; IPR001751; CaBP_S100.
InterPro; IPR002048; EF-hand.
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Pfam; PF01023; S 100; 1.
ProDom; PD003407; CaBP S100; 1.
ProDom; PD000012; EF-hand; 1.
PROSITE; PS00018; EF HAND; 1.
PROSITE; PS000303; S100 CABP; 1.
SEQUENCE 101 AA; 11847 MW; 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 52.
Thes 31; Conservative 7.
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                            EMBL; AL356504; CAC13172.1;
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Best Local Similarity 34.5%
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                PIR; A48118; A48118.
HSSP; P80511; 1E8A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              687 AA;
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TISSUE-FORESKIN;

X MEDLINE-93109348; PubMed=8417356;

A MEDLINE-93109348; PubMed=8417356;

A Steinert P.M.;

"Profilaggrin is a major epidermal calcium-binding protein.";

"Profilaggrin is 613-625(1993).

-!- FUNCTION. AGGREGATES KERATIN INTERMEDIATE FILAMENTS AND PROMOTES

DISULFID-BOND FORMATION AMONGST THE INTERMEDIATE FILAMENTS DURING

TERMINAL DIFFERENTIATION OF MAMMALIAN BFIDERMIS.

-!- FTM: FILAGGRIN IS INITIALLY SYNTHESIZED AS LARGE, INSOLUBLE,

HIGHLY PHOSPHORYLATED PRECURSOR CONTAINING MANY TANDEM COPIES OF

324 AA. THE PRECURSOR IS DEPOSTIED AS KERATOHYALIN GRANULES.

DURING TERMINAL DIFFERENTIATION IT IS DEPHOSPHORYLATED &

PROTEOLYTICALLY CLEAVED.

PROTEOLYTICALLY CLEAVED.

-!- POLYMORPHISM: A NUMBER OF PROFILAGGRIN ISOFORMS HAVE BEEN FOUND

WHICH DIFFER BOTH IN SEQUENCE AND IN THE NUMBER OF FILAGGRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M GO; GO:0005865; C:cytoakeleton; NAS.

RGO; GO:0005809; F:calcium ion binding; TAS.

RGO; GO:0005154; P:cell differentiation; NAS.

RGO; GO:0008151; P:cell growth and/or maintenance; NAS.

RGO; GO:0008151; P:cell growth and/or maintenance; NAS.

RICEPTO; IPR0021031; CaBP S100.

RICEPTO; IPR003103; Filaggrin.

R Pfam; PP001021; Filaggrin.

R Pfam; PR001021; S 100; I.

R PRINTS; PR004807; PILAGGRIN.

R PROSITE; PS00018; EF HAND; I.

R PROSITE; PS00018; EF HAND; I.

R PROSITE; PS00018; EP HAND; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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1218 AA; 133604 MW; EC195AD5285B19C2 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
FILAGGRIN (PROFILAGGRIN) (Fregment).
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                                                                   63 NODEQUSFKEFUVLUTDVLITAHD 86
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EMBL; M96943; AAA36487.1; -.
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Search completed: March 5, 2004, 09:48:53 Job time : 40 secs

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Homo sapi Rattus no

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AC023796 AC024025 AC092867 AC095169

ALIGNMENTS

Homo sapi

Continuation (12 o AL590227 Human DNA AL591594 Human DNA

PFMAL13 11 AL590227 AL591594

AX541172 AX541169

AX541247

AC078940

Sequence Sequence

AX541247 Sequence

Homo sapi Canis fam Zebrafish

AC007068 ]

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AL357124 AC116330

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AC122143 AL159152 AX541033

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AC112251 Homo sapi AY303349 Enterobac AC021473 Homo sapi AC097467 Homo sapi

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AC133975 | AF267206 (

Z93373 Caenorhabdi AL008970 Plasmodiu AC099283 Rattus no

51 Homo sapi Caenorhabdi

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AF288092 NAC004453 B

AC021473 AC097467 AF288092

AC146064 AC105564 CEY41E3 AC007068 AC121076

AC004453

PAT 26~JAN-2000 linear (Cabes 1 to 298)

Koch-Pelster, B. and Kuhn, E.
RIBONUCIBGTIDE POLYPEPTIDES CONTAINING METAL
ROCH PELSTER BYJ561-A 3 23-SEP-1999;
KOCH PELSTER BRIGITTE (DE); KUHN ECKEHARD (DE) DNA Sequence 3 from Patent W09947561. 294582 GI:6778899 unidentified unclassified. unidentified A94582.1

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159690 AAAAAATCATATTATGTATAATCTTTTTTTTTTGGTGACGGGGGGAAAAGGATGCTT 159631
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Human chromosome 14 DNA sequence BAC R-36986 of library RPCI-11
from chromosome 14 of Homo sapiens (Human), complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 167398)

Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P., Brottier,P., Cattolico,L., Barbe,V., Pelletier,B., Artiguenave,F., Gyapay,G., Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (28-APR-2001) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The following BAC sequence is oriented from the T7 to the SP6 end.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - Web : www.genoscope.cns.fr)
On Apr 30, 2001 this sequence version replaced gi:11181947.
                                                                                                                                                                                                                                                                                                                              dbSTS:STS817
Identified using the e-PCR software (G. Schuler)"
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                                                                                                                                                                                                                              e-PCR software (G.
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22.1%; Pred. No. 1.3e+02;
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                                                                                                                                                                  /note="matching EMBL:N74379 RHdb:RH91341
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/note="matching EMBL:G03450
RHdb:RH53483
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                                /organism="Homo sapiens
mol_type="genomic DNN"
/db_xref="taxon:9606"
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Location/Qualifiers
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Human chromosome 14 DNA sequence BAC R-533L7 of library RPCI-11
from chromosome 14 of Homo sapiens (Human), complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (02-MAY-2001) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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[ (bases 1 to 162986)]

Heilig, R., Petit, J.L., Vico, V., Dasilva, C., Robert, C., Wincker, P., Brottier, P., Cattolico, L., Barbe, V., Pelletier, E., Artiguenave, F., Gyapay, G., Saurin, W. and Weissenbach, J.

Sequencing of the human chromosome 14
                                                                                                                                                                                                                                              ::
TTTGTACATAAAAATAAAAACATGACTTCTTTAGACACTCCTTCATTAGAATAAAATAA 148
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                                                                                                                                                                                                                  16
                                                                                                                                                                                                                  Gaps
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On Jan 1, 2001 this sequence version replaced gi:7768128.
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                                                                                                                                        Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assembly program: Phrap; version 2.0 Quality coverage: 8.81x in Q20 bases; sum-of-contigs
                                                                                                                                                                              44; Indels
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                                                                                                                                      29.3%; Score 31.4; DB 6;
llarity 30.3%; Pred. No. 3.7e+02;
Conservative 9; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.genoscope.cns.fr/
Contact: SegRef@genoscope.cns.fr
                                          /organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -- Summary Statistics
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    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                  92 NNNNNNNNNNUAGCAG 107
                                                                                                                                                                                                                                                                                                                                      149 AATAAACTATTÄGCÄG 164
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Homo sapiens
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                                                                                                                                        Query Match
Best Local Similarity
Matches 23; Conserv
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Gaps

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This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurachly this particular cDNA clone. However, there are artifacts associated with the generation of CDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to erverse transcription of unspliced precursor RNAs, and reverse transcription of unspliced precursor RNAs, and reverse transcription about this sequence, including its location and relationship to other sequences, please visit our Web site (http://fruitfly.berkeley.edu) or send email to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSRSSPERDSLVRLSQRRPDLVDAQYTILATDADPVEKMPLVEHCQFKYLFNFRGVAA
SFRLRHILLCRSLVLHVGDQWQEFFYSQLKPWVHYVPVASDADVDELAELILYLREHD
DLAEEIAERGQQFIWLHLRMEDVQCYWSKMLQEYAKLLTYKVQREPGLLEVSNKKAVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAN71037.1"
/db_xref==[G1:25009725"
/db_xref="FLYBASE: BBGRO039021"
/db_xref="FLYBASE: BBGRO039021"
/translation="MTQPRICFLVGALILSCTCVSCSKDKCAAIEHNPNSNTSYDFVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HILHALAIHRPCVIGDPKCLCHVATIQRDLEPYVDKGITPEMMAQSKRLGTFYQIIRG
RIYRQQKCLHPKRCADVEDLLLDMASGVADLEFVLNVRDWPQVHFLSGLSGPVFSYSI
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Cancer Institute Human
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  Direct Submission
Submitted (15-NOV-2002) Berkeley Drosophila Genome Project,
                                         Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 9420, USA
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
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26.5%; Pred. No. 5.8e+02;
iive 12; Mismatches 49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="CG17138"
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Homo sapiens
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Best Local Similarity
Matches 22; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identified using the e-PCR software (G. Schuler)"
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Drosophila melanogaster AT07872 full insert cDNA,
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Identified using the e-PCR software
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="matching EMBL:N74379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="matching EMBL:G03450
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FLI CDNA.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic_DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="R-369B6"
/clone_lib="RPCI-11"
90076._.90202
                                                                                                                                                                                                                                                                                                                                                                                                                          chromosome="14"
                                                                                                                                                                                                                                                                                                                                                               ordanism="Homo
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                                                                                                                                                                                                                                                                                              Percentage
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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones.

Overlapping clones are noted at the beginning and end of the Features listing.

us-09-646-651c-2.rge

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REFERENCE
          AUTHORS
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Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 133636)

AUTHORS TITLE JOURNAL REFERENCE

Vorley, K.C.
Direct Submission

Direct Submission

Submitted (10-APR-2002) Human Genome Sequencing Center, Department

Submitted (10-APR-2002) Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA (bases 1 to 133636) REFERENCE

Submitted (29-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA Baylor Plaza, Houston, 4 (bases 1 to 133636) Worley, K.C. Direct Submission Worley, K.C. Direct Submission

TITLE JOURNAL

AUTHORS

TITLE JOURNAL

REFERENCE AUTHORS

Submitted (01-0CT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA ON Sep 30, 2002 this sequence version replaced gi:21553164. GINFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu Submitted (30-SEP-2002) Human Genome Sequencing Center, Departmen of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 133636) Worley, K.C. Direct Submission

TITLE JOURNAL REFERENCE AUTHORS

COMMENT

/rpt\_family="AluJb"

/rpt\_family="L1ME complement(10579.

repeat\_region repeat\_region

CE MULTAY, D.M., Adams. C., Adio-Catola, B. Ali-cemenn, F.R., Allen, C., Alian, C. Adio-Catola, B. Ali-cemenn, F.R., Allen, C., Alian, C., Adio-Catola, B. Ali-cemenn, F. Brownin, D. Barbaria, J., Berde, S., Brieva, M., Brown, B., Brown, M., Barwai, T. Barbaria, J., Berden, J., Elmage, K., Blankenburg, K., Bonnin, D., Butch, J., Brieva, M., Brown, B., Brown, M., Bryant, N.C., Carron, T., Burton, P., Shretch, C., Burrell, K.L., Byrd, N.C., Chen, G., Chen, G., Erter, M., Cavacos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, C., Day, Carroll, L., Dederich, D. A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Ding, Y., Dind, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinch, H.H., Douthwalter, K.J., Draper, H., Dugan-Rochas, S.R., David, K.J., Barnlart, C., Edgar, D., Edwards, C.C., Elhaj, C., Becotto, M., Farnlact, C., Edgar, D., Edwards, C.C., Elhaj, C., Becotto, M., Farnlact, C., Harris, K., Har, M., Havlak, P., Hale, S., Hamilton, K., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Harris, K., Harris, K., Harris, K., Harris, C., Harris, K., Harris, C., Harris, C., Harris, K., Harris, C., Harris, K., Harris, C., Harris, M., Hollows, M., Hollows, C., Karlsson, E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Jacobson, B., Jia, Y., Johnson, R., Molte, S., Martinez, E., Mascado, R., Li, Ju, Y., Ludier, M., Mallyk, S., Martinez, E., Mascado, R., Martin, R., Mart Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage. "Merchait are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts. flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar. ANNOTATION OF FEATURES:

http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found

/rpt\_family="LiM4c" complement(10094. 10457) /rpt\_family="LiME" complement(10456. 10578) family="Limbc" ement(10=7) . .197 |standard name="RH122785" /rpt\_family="(TA)n" complement(9405, ,9825) 1. .133636 /organism="Homo sapiens .9207) /mol\_type="genomic\_DNA" /db\_xref="taxon:9606" /rpt\_family="HERVK\_9" 8313, .8845 complement (513. .810) /rpt\_family="AluSx" 'rpt\_family="AT\_rich" 599. .1747 rpt\_family="MER46C" 794. .2232 rpt\_family="(TG)n" 254. .2310 /rpt\_family="LlM4c" 9225. .9396 clone="RP11-69K16" rpt\_family="AluJb" 423. .1453 Location/Qualifiers /rpt\_family="MER9" 8037. .8312 rpt\_family="MER9" 233. .2253 /rpt\_family="MER9" complement(8886... chromosome="3" repeat\_region repeat region source FEATURES

us-09-646-651c-2.rge

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Submitted (05-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, CBIO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk clone Apr 6, 2001 this sequence version replaced gi:13273767.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations. Where differences are found these are annotated as variations. Where differences are found the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMEL; Sw:, SWISSPROT; Tr:, TREMEL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/HGP/Chr13
RP11-431P10 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sections only once, except for a 100 base overlap.

The true right end of clone RPI1-431R10 is at 86050 in this sequence. The true left end of clone RPI1-569012 is at 48980 in this sequence. The true right end of clone RPI1-600P1 is at 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4530. .6107
/note="LiPAl5 repeat: matches 4541. .6157 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone
RP11-431P10 It may be shorter because we sequence overlapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .568 of consensus"
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/note="25 copies 2 mer gt 78% conserved"
8343. 8653
/note="Alusx repeat: matches 1. .311 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .3743 of
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/note="L1MEc repeat: matches 1479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3270. .4102
/note="L1MEc repeat: matches 1695.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9055. ,9356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /chromosome="13"
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/clone=lib="RPCI-11.2"
/clone=lib="RPCI-11.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'organism="Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic_DNA"
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Human DNA sequence from clone RP11-431P10 on chromosome 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.9%; Score 29.8; DB 9; Length 133636; 23.4%; Pred. No. 1.6e+02; ive 12; Mismatches 70; Indels 0;
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1.6e+02;
70;
                                                                        name="SHGC-77614"
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15616. 15945
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                                                                                                                                                                                                                                                                     rpt family="L1PB3"
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2553. .22717
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3205. .23829
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2243, 225er
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9697. .20414
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complement(24162.
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0697. .21004
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3799. .24083
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24456. .24795
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                                                                          /standard
12033. .1<u>2</u>
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Best Local Similarity 23.44
Matches 25; Conservative
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/note="match: GSS: Em:AQ728730"

10260. ,10779 /note="match: GSS: Em:AQ804059" 11538. ,11837

repeat\_region

misc\_feature

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Homo sapiens (human)

EFINITION

CCESSION TERSION CEYWORDS

RESULT 6 NL359647 OCUS

አ

Homo sapiens

ORGANISM

OURCE

EFERENCE

Mammalia; Butheria; Primates; Catarrhin; Hominidae; Homo. 1 (bases 1 to 86050) Phillimore, B.

note="match: GSS: Em:AQ215557"

.10707

```
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17069. "17312
/note="MinJb repeat: matches 5. 259 of consensus"
17500. "18043 repeat: matches 5. 259 of consensus"
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/note="match: GSS: Em:AG019010"
/note="match: GSS: Em:AG37557"
18139. "18182
/note="match: GSS: Em:Ag37557"
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/note="LiPAl5 repeat: matches 5791. .6157 of consensus"
24445. .24663
/note="AluJo repeat: matches 22. .244 of consensus"
26108. .26517
/note="MRR57A repeat: matches 1. .426 of consensus"
/note="MRR57A repeat: matches 1. .188 of consensus"
/note="MRR57A repeat: matches 1. .188 of consensus"
27390. .26487
/note="LiPA3 repeat: matches 5044. .6146 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18711. .19930
/note="Tigger3b repeat: matches 3. .1231 of consensus"
/note="LiMA9 repeat: matches 5329. .5365 of consensus"
/note="MLIMA1 repeat: matches 3. .365 of consensus"
/note="MLIMA1 repeat: matches 3. .365 of consensus"
20363. .22158
/note="LiMA9 repeat: matches 3600. .5329 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .5014 of consensus"
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15127. .15370
/note="L2 repeat: matches 790. .1041 of consensus"
15357. .15894
/note="L2 repeat: matches 2156. .2717 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                              .5929. .16389
hote="L2 repeat: matches 1057. .1516 of consensus"
6582. .16879
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/note="THE1B repeat: matches 1. .364 of consensus"
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/note="AluY repeat: matches 3. .302 of consensus"
11838. .11873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of
                                             /note="12 copies 3 mer taa 100% conserved"
14096. .14213
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/note="L1PA3 repeat: matches 4286.
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                                                                                                                                                                                          'note="MLT1A2 repeat: matches 4.
                                                                                                                                                                                                                                     /note="match: GSS: Em:AQ694000
|5052. .15118
                                                                                           /note="match: STS: Em:G19980"
14097. .14420
                                                                                                                                         /note="match: STS: Em:G06796"
14676. .14943
                                                                                                                                                                                                                  . .15135)
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Methanococcus jannaschii section 81 of 150 of the complete genome.
U67539 L77117
U67539.1 GI:1591619
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Bult, C.J., White, O., Olsen, G.J., Zhou, L., Fleischmann, R.D.,
Sutton, G.G., Blake, J.A., FitzGerald, L.M., Clayton, R.A.,
Gocayne, J.D., Kerlavage, A.R., Dougherty, B.A., Tomb, J.,
Relch, C.I., Overbeek, R., Kirkness, E.F., Weinstock, K.G.,
Merrick, J.M., Glodek, A., Scott, J.D., Geoghagen, N.S., Weidman, J.F.,
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//note="MLTIC repeat: matches 6. .466 of consensus"
45290 ...#5388
//note="L2 repeat: matches 1662...1748 of consensus"
45389...#5881 ...#5889
//note="MLT2PA repeat: matches 1. .448 of consensus"
45864...#6154
//note="MLT2PA repeat: matches 1748...2097 of consensus"
46192...#6114
//note="MLT1B repeat: matches 154...390 of consensus"
46415...#6717
//note="MLT1B repeat: matches 1...307 of consensus"
46415...#6803
//note="MLT1B repeat: matches 1...307 of consensus"
46718...#6803
//note="MLT1B repeat: matches 112...154 of consensus"
                                                         .6145 of consensus"
                                                                                                                                                      consensus"
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                                                                                                                                                                                                                                                                                                                                    consensus"
                                                                                                                                               /note="Limas repeat: matches 6199. .6300 of consens: complement (3849. 34245)
/note="match: GSS: Em:B32835"
/note="L2 repeat: matches 2561. .2690 of consensus"
34745. .34809
/note="Mill repeat: matches 71. .134 of consensus"
34839. .37202
/note="TiggER1 repeat: matches 1. .2414 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                            .2489 of consensus"
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Methanocaldococcus jannaschii
Archaea: Euryarchaeota; Methanococci; Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
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72535 TGTAGAGTTCTTAGCAATAGAATATGATTATCTATTATTT 72576
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                                                                                                          .5333
             /note="33 copies 2 mer cc 68% conserved"
32542. .33345
                                                                                                                                                                                                                                                                                                                                                         40465. 40878
/note="match: GSS: Em:AQ109183"
41540. 41641
/note="L2 repeat: matches 2397. 248
42086. 42218
42489. 42816
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                                                            /note="L1PA5 repeat: matches 5342.
33346. ,33572
                                                                                                          5107.
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ilarity 21.6%; Pred. No. 2e+02;
Conservative 13; Mismatches 67;
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44832. .45269
                                                                                                        /note="L1PAS repeat: matches 33723. .33822
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Best Local Similarity
Matches 22; Conserv
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U67539
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FATURES

COMMENT

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/codon_start=1
/transT_table=11
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/product=iM-, jannaschii predicted coding region MJ0956"
/protein_i="Ma" AAB9869.1"
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AVTFISDRSPKWYREETRAIMMANDYHRFTECGKCKISLENNGHDYHGSCVWHEGTR
NFBGGVVASSIGEHIKDKERFLTWCNDYNLFEPFIHLNVSRERLVKEFESLDKNLISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNENPWGPSPKIKEKILDBIDKIHQYPEPVNPILMKELSKFLNVDEENIIVGGGGDE
IIDTIRRTFVDDGDEVIIPIPTTOYRVSATIHNAKIKYAKYDKEKDFKLAVUSSVLAN
ITDKTKVIFLCTPNNPTGNIIENRDVERVINETDBALVIDHAYIRYAKKEYDWTGRAP
BYDNVIVLRFSKVFGLAGMRVGYGVANKKIIDYMMRVEPIFSLITKLSQVCAITALRD
REPFRCYRDGIKSREMLYMGLKFKDIKVYPSEANYLLYDEKTHKRAKEFCEELLKRG
VIVRDCTSFDGLGDNYVRVSIGTFEEVERFLKILEEIIS"
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GRLSNTSFPLYSYYGGK.HFEDNITLPKYENISWECNDFYSINGTLYIVOKKLINCSNI
NYAGWYEDYLIOKPYLLIWNYTIXIISNCSNPYYFVKIKGGEIPIEKSYLKKIFGNK
YESIRITDLAYNUGILLETNENHKLHYYIVKONSIEEIKLKNIIKLYKKKGHSLWDDI
KKELEPKIYWVIHNWYIIVLIAGLLWMAILWKK"
                                                                                                                                                                                                                                                                                                                                                      /producE="M. jannaschii predicted coding region MJ0957"
(protein id="AhB98970.1"
(db_xref="GI:1499794"
(translation="MGDDIYIPPKEPKPKPKPEYKYALWYFKYTNIYEKRFNGTVGD")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGQVSWGFITDWBIAQLSTYIKQKSNELNRKLEFIWIPYINDIENPDNNDIKRLSKYF
DYVFVQPHYYIAWKYWCLMNYEKNVSEDIREYWKYQINRYNGYLIQGITKLIEVLNWI
KEIPNGYIEMEVDNKIDEYKYHDLINKACDYIKAREFLIGRDIWQIRAYYFDTNIENV
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VKIYYNKYIRELDEPYADYIKSRDVEMFDKLVNKCKEYLGVK"
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RGMLEKLKNASKDKKQMEYYINHIYLVKRTLEYWKGWIDGVI ESCDSNLVGFYMNFES
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/db_xref="GI:1499795"
/translation="MKKFILFLIILLFSIYPLNVSSAEVCPFKDGFIIIYHDIGYDKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FGYTYNDSELLYFNNKNLMDITPISDYYFPELYHNITYFECGSTNNLTILSFGXFFP
KNGDGIVFLGVLVYTTKNNKINYTEKILMADVFYSVDDFDISPPACSPNEALLVYCYK
                                                                                                                                                          /note="similar to SP:P06986 GB:U02071 GB:X03416 PID:41695 PID:41710 percent identity: 29.00; identified by sequence
                                                                                                                                                                                                                                                                                                                           'product="histidinol-phosphate aminotransferase (hisC)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4427. .5479
/gene="MJ0957"
4427. .5479
/gene="MJ0957"
/note="hypothetical protein; identified by GeneMark;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="MJ0956"
3645. .4427
3645. .4427
/note="MJ0956"
/note="hypothetical protein; identified by GeneMark;
putative"
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/note="hypothetical protein; identified by GeneMark;
PYNDNNIYILAGSDRWGTKAAILVFLTKYNDEDTLMVEWDKGEIKIIK"
                                                                                                                                                                                                                                similarity; putative"
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/transl_table=11
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                          2378. .3499
/gene="MJ0955"
                                                                                             2378. .3499
/gene="MJ0955"
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HTG 16-NOV-1999

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1600001 1664976
of AR271569 from base 500001 (AR271569 Sequence 1 from patent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 AAAAUNNININUNAUAUGININININCUNNINUUUNINININAAAAANUANAAACAUNININININCUU
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Drosophila melanogaster
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
1 (bases 1 to 60471)
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Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          by the finished sequence as soon as it is available and the accession number will be preserved.

Location/Qualifiers
                                                                      Length 110000;
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                                                                                                                                                                                                                                                                                                                                            bp DNA linear
SEQUENCING IN PROGRESS
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* NoTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finish.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
                                                                                                         69
                                                                    Score 29.4; DB 6;
Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 29.2; DB 2;
Pred. No. 2.7e+02;
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                                                                                                         10; Mismatches
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1610000
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AC015173.1 GI:6436162
HTG; HTGS PHASE2
Drosophila melanogaster (f
Drosophila melanogaster
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                                                                    27.5%; 24.8%;
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25.0%;
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AR271569_16
Continuation [6 c
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Best Local S
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AC015173/c
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AC009846/c
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NDTVGSYLDLAYKKYTEEKÇTPYTPSVNLTYALNVALDLUJEGTENRVKHERLA
KATRAGLEAMGIELFAKERARSVTVTSAKYPEGIEDSKFRGILSNKYNIVVAGGQKHI
AGKIFRIGHNGICGEKEVLATLACVELALKELGFEVKESGVEVAKEVLKE"
complement (7990. .8643)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EICEIVEGPVSAEVISTDAEGMVKEARELAKLADNIVIKIPMTKDGMKAVKILSAEGI
KINVTLVFSPLQALVAAKAGATYVSPFVGRLDDIGHVGMKLIEDVVKIYKNYDIKTEV
IVASVRHPMHVLEAAKIGADIATMPPAVMDKLFNHPLTDIGLERFLKDMDEYLKSRK"
                                                                        PID:704449 GB:AE000666 percent identity:
by sequence similarity; putative"
                                                                                                                                                                                                  /tränslation="MKIDAVKKLIMIPGPTMVPPEVLNAMALPVIGHRTKDYSNLLED
TIEKLKKVFITENDIFLITGSGTAAMDMAISNIIKRGDKVLNIVTGNFGERFANIVKA
                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to SP:P19669 PID:853766 GB:AL009126 percent
identity: 59.02; identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                      YKGEAIRLDVEWGDMAEPEAVKEILDKYDDIKAVTVVHNETSTGARNPIKEIGEVVKD
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note="similar to SP:P30665 PID:1314093 PID:3482
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                                                                                                                                 /product="aspartate aminotransferase (aspC) /protein_id="AABB961.1" /db_xref="G1:1591623"
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24.8%; Pred. No. 3.5e+02;
iive 10; Mismatches 69;
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/protein_id="AAB98962.1"
/db_xref="G1:1591624"
 complement (6788. .7945)
                  /gene="MJ0959"
complement(6788. .7945)
                                                                                                                                                                                                                                                                                                                                                                    complement (7990. .8643)
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                                                                        /note="similar to
54.69; identified
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8860. .11148
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AR271569 00
AR271569 03
AR271569 03
AR271569 06
AR271569 06
AR271569 07
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AR271569_10
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Best Local S
Matches 26
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AR271569 05/c
WPCOMMENT
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the submitter. to fly@celera.com.

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Gaps

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SPERENCE AUTHORS

GI:23171988

AE003740.3

VERSION

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REFERENCE
AUTHORS
                                                                                ORGANISM
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AUTHORS
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                     KEYWORDS
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                                                 SOURCE
       Locates 1 C. Ladams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,
Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,
Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C.,
Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A.,
Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M.,
Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D.,
Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A.,
Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J.,
Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A.,
McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J.,
Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B.,
Phousneavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F.,
Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M.,
Sequencing of Drosophila chromosome 3R, region 94C-94D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence)) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (03-SEP-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA on Feb 17, 2001 this sequence version replaced gi:6957584.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGAAAAUNNNNNNAUAUGNNNNNNNCUNNNNTUUUNNNNNNAAAAANUANAAACAUNNNNNC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Letter, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Houston, R.A., Humasti, S.R., Karraw, R., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Sequeira, A., Sethi, H., Shir, E., Svirskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zleran, L.L. and
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Drosophila melanogaster BAC library, partial EcoRI in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Drosophila melanogaster"
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Best Local Similarity
Matches 21; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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Epydrotolasi, Drosophilidas; Drosophilia.

Epydrotolasi, Drosophilidas; Drosophilia.

Edydrotolasi, Drosophilidas; Drosophilia.

Edwams, M.D., Celniker, S.E., Hid.P.W., Hoskins, R.A., Galle, R.F., Gamanides, P.G., Schere, S.E., Li, P.W., Hoskins, R.A., Galle, R.F., Garten, G.W., Gruman, J.R., Yandell, M.D., Zhang, Q., Chan, L.X., Brandell, M.D., Zhang, Q.C., Ghan, L.X., Brandell, M.D., Zhang, Q.C., Gabrer, G.L., Man, H.J., Andell, J., Baylash, P. Felffer, B.D., Abril, J.F., Apdrayan, A., An, H.J., Anderse-Frankoch, C. Baldwin, D. Ballew, R.W., Basu, A., Bardell, J., Bayraktaroglu, L., Beasley, E.M., Beson, K.Y., Benos, P.V., Bernan, B.F., Bandari, D., Bolhakov, S., Borkchan, M.Y., Bouck, J., Broketen, P., Erottier, P., Bortchan, M.Y., Bouck, J., Broketen, P., Crettier, P., Burdar, D.A., Butler H. G., Cahley, S., Dalke, C., Davenport, L.B., Davies, P., de Pablos, B., Delcher, A., Deng, Z., Nays, A.D., Dew, I., Dietz, S.M., Dodson, K., Dolle, E.E., Downes, M., Dugan-Rocha, S., Dunkov, B.C., Dunn, P., Dulchier, A., Browes, M., Dugan-Rocha, S., Cherriera, S., Fleischmann, M., Fosler, C., Gabriellan, E., Garell, J. H., Gu, Z., Guan, P., Harris, M. M., Glasser, K., Glodek, A., Gong, F., Gorrell, J. H., Gu, Z., Guan, P., Harris, M. Lin, X., Haush, F., Karpen, G.H., Ke, Z., Kannison, J.A., Ketchum, K.A., Kimmel, B.E., Kodira, C.D., Kraft, C., Morriera, M., Mourt, S.M., Moy, M., Murphy, B., Murphy, B., Murphy, B., Murphy, B., Murphy, D., Mal, M., Dellard, J., Liu, X., Liu, X., Mattei, B., Wolland, C., Pollard, J., Moshrefi, A., Mount, S.M., Moy, M., Murphy, B., Worler, M., Strong, R., Sun, H., Shee, R., Spradling, A.C., Stapler, C., Woller, S., Shen, H., Shen, H., Shen, R., Spradling, A.C., Stapler, M., Worles, M., Worles, M., Worles, M., Worles, M., Strong, R., Sun, H., Shen, R., Spradling, A., Shen, R., Shen, R., Spradling, A., Chan, M., Strong, R., Shen, H., Shen, R., Spradling, A., Shen, R., Shen, R., Shen, R., Shen, R., Shong, S., Woodeger, The genome sequence of Drosophila melanogaster. The genome sequence of 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Celniker, S.E., Adams, M.D., Kronmiller, B., Wan, K.H., Holt, R.A., S. Capars, C.A., Amanatides, P.G., Brandon, R.C., Rogers, Y., Buans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y., Bancs, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Busam, D.A., Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferriera, S., Frises, E., Galle, R.F., Garrg, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J., Parksagas, V., Parks, S., Patel, S., Pfeiffer, B., Pacagas, V., Parks, S., Patel, S., Pfeiffer, B., Scheeler, F., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Tyler, D., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Tyler, D., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Tyler, D., Stapleton, S., Scheeler, S., Scheeler, S., Scheeler, S., Sequencing of Drosophila melanogaster genome
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Drosophila melanogaster (fruit fly)
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Homo sapiens 12g BAC RP11-346L11 (Roswell Park Cancer Institute
Human BAC Library) complete sequence.
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(bases 1 to 234378)
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Submitted (13-FEB-2003) University of California Berkeley, 539 Life
Sciences Addition, Berkeley, CA 94720, USA
Sequence update by submitter
On Sep 18, 2002 this sequence version replaced gi:10726705.
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18885. . 19523
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                                                                                                       4 (bases 1 to 234378)
Adams,M.D., Celniker,S.E., Gibbs,R.A., Rubin,G.M. and Venter,C.J.
Direct Submission
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[3311, .13380]
locus_tag="CG17622"
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/note="genotype: y[1]; cn[1] bw[1] sp[1]; Rh6[1]"
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/note="last curated on Tue Jan 22 00:33:38
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join[18885..18931,19007..19523)
/locus tag="CG17623"
         Rubin, G.M., Mungall, C.J. and Lewis, S.E.
Annotation of Drosophila melanogaster genome
Unpublished
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/organism="Drosophila melanogaster"
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'db xref="GI:23171989"
'db_xref="FLYBASE:FBgn0038999"
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Rockville, MD 20850, USA
5 (bases 1 to 234378)
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                                                      Manmaliai inclease; Primates; Catarinini; Honinidae; Homo.

(bases it to 1919,9)

Muzny, D.M., Adams, C., Adio-Odoloja, B., Ali-Osman, F.X., Allen, C.,

Alabrooks, S.L., Amaturge, H.C., Are, J.R., Banke, T., Barke, T.,

Burch, D., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J.,

Burch, E., Britara, M., Brown, E., Brown, M., Bryatt, NP., Burket, C.,

Burch, D., Burket, C., Burneil, K.L., Byrd, N.C., Carron, T.F.,

Carter, M., Cavaces, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R.,

Carter, M., Ding, Y., Dathorne, S.R., David, R., Davila, M.L., Davis, C.,

Dany, Cartoll, L., Dederich, D.A., Delaney, K.R., Delagato, D.,

Cox, C., Coyle, M.D., Dathorne, S.R., Davintat, C., Edgar, D., Edward, C.D.,

Dany, Cartoll, L., Dederich, D.A., Delaney, K.R., Deper, H.,

Dugan, Rocha, S., Durbin, K.J., Barnhart, C., Edgar, D., Edward, C.C.,

Ellaj, C., Emerling, S., Beccotto, M., Falls, T., Ferragoto, D.,

Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, D.,

Flagg, N., Ford, J., Hule, S., Hamilton, K., Harnis, C., Harris, K.,

Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W.,

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Howard, S., Huber, J., Hulyk, S., Hume, J., Toshkhesi, I., Gackeon, L. B.,

Jacobson, B., Jai, Y., Ohlivet, S., Joudah, S.,

Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,

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Martindale, A., Martinez, E., Massey, E., Mawhiney, E., Mcicod, M. P.,

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Shoosher, M., Stsonl, I., Sodergram, E., Sont, G., Shork, P., Put, L.,

Quiles, M., Rallsky, R., Shork, M., Syatek, A., Polubokan, I. Telfrod, B.,

Thomas, N., Thomas, S., Usher, M., Will, Y., Wu, C., Yu, Villalon, Niyer, Niyer, N
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4 (bases 1 to 191942)
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Submitted (09-AUG-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Ravlor Plaza, Houston, TX 77030, USA
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INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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gc-help@bcm.tmc.edu
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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

## ANNOTATION OF FEATURES:

STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the BST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the SEQUENCING READ COVERAGE: Sequencing is completed to a minimum annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html

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QUALSTAT-REPORT
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OMMENT

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INFORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlapping sections once, or longer because we arrange for a small this sequence is the entire insert of clone C01B9. The true left end of clone ZK131 is at 18285 in this sequence. The true right end of clone R06B9 is at 100 in this sequence. The start of this sequence (1. 100) overlaps with the end of sequence CER06B9.

The end of this sequence (24951, .25233) overlaps with the start of sequence CEZK131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23035 ATAAGCTTGCTAATTTTTTCTGGCTTTTTTTAAATAGAAATATAGAAAATATAGGAAATATCGGCTG 22976
                                                                                                                                                                                                                                                                                                                                                   s, using other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INV 29-JAN-2003
                                                                                                                                                                                                                            Submitted (27-MAR-1997) Nematode Sequencing Project, Sanger
Institute, Hinxton, Cambridge CB10 1SA, England and Department of
Genetics, Washington University, St. Louis, MO 63110, USA. B-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bowman, S., Lawson, D., Basham, D., Brown, D., Chillingworth, T., Churcher, C.W., Craig, A., Davies, R.M., Devlin, K., Peltwell, T., Gentles, S., Gwilliam, R., Haulin, N., Harris, D., Holroyd, S., Hornsby, T., Horrocks, P., Jagels, K., Jassal, B., Kyes, S., McLean, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note. For a graphical representation of this sequence and its analysis see:- http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence? name=C01B9
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                                                                                                                                                                                                                                                                                                                                                                                           available information.

Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a
                                                                                                                                                                                                                                                                                                                         On Jun 13, 1998 this sequence version replaced gi:1913957.
Coding sequences below are predicted from computer analysis,
predictions from Genefinder (P. Green, U. Washington), and ot
                     Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium falciparum 3D7
plasmodium falciparum 3D7
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 113880)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22975 GAGTITAAATITICIGAGAAAATITITIGGCGGGAATITITA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Caenorhabditis elegans"
                                                                                                                                                                                                                                                                                                 jes@sanger.ac.uk or rw@nematode.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 28.6; DB 3;
; Pred. No. 4.9e+02;
12; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA
                                                                                                                                    The C.elegans Sequencing Consortium. 2 (bases 1 to 25233)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="Bristol N2"
/db_xref="taxon:6239"
/clone="C01B9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113880 bp
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AL008970 AL139179 AL844502
AL008970.3 GI:7672212
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ilarity 21.8%;
Conservative 12
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                                                                                                                                                                                                            Direct Submission
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Best Local Similarity
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ACCESSION
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ORGANISM
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                                                                                          MEDLINE
PUBMED
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AUTHORS
                                                                                                                                                                                  AUTHORS
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                                                                  JOURNAL
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                              COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155959 GGAGAATGAAATTAACTTTTTCTGTCTGGATTTAGGAGAAACAATGGAAACATTTAAA 156018
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'note="Region: HSLACTG Human alpha-lactalbumin gene"
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Caenorhabditis elegans
Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida,
Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CECO1B9 25233 bp DNA linear INV Caenorhabditis elegans cosmid CO1B9, complete sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 191942;
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23.3%; Pred. No. 2.2e+02;
ive 11; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26062. .26197

/rpt_family="LilMA9"

/sofe. .2637

/rpt_family="Alusq"

complement(27254. .27352)

/rpt_family="MIR"

complement(27254. .2822)

/rpt_family="MIR"

complement(27952. .28222)
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31469. .31773
/rpt_family="AlluJb"
complement(32145. .32452)
/rpt_family="AlluSx"
                     complement(16729. .17246)
/rpt family="HUBRS-P3b"
                                          /rpt_family="HUERS-P3b"
complement(17247. .17899)
/rpt_family="LTR9B"
                                                                                            19794. 20065

/ rpt_family="AluJb"

21526. 21568

21526. 21568

21589. 21885

/ rpt_family="MIR"

21589. 21885

/ rpt_family="AluSx"

22537. 22570

/ rpt_family="(TAAA)n"

22606. 22591

/ rpt_family="MIR"

24268. 24518.
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30486. .30515
/rpt family="(CATA)n"
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26062. .26107
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/rpt_family="AluSq"
25352. .25640
                                                                                                                                                                                                                                                                                                                                                               /rpt_family="Alusc"
24566..24738
/rpt_family="FAM"
24925..24990
25052..25349
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Z93373.1 GI:3217060
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Best Local Similarity 23.3%,
...hes 24; Conservative
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KEYWORDS
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                                                                                                                                                                                                                                                                              Hall, N., Pain, A., Berriman, M., Churcher, C., Harris, B., Harris, D., Mungall, K., Bowman, S., Atkin, R., Baker, S., Barron, A., Brooks, K., Bucke, C.O., Burrows, C., Chereveach, I., Chillingworth, C., Chillingworth, T., Christodollou, Z., Clark, L., Clark, R., Corton, C., Cronin, A., Davies, R., Davis, P., Dear, P., Dearden, F., Doggett, J., Feltwell, T., Goble, A., Goodhead, I., Gwilliam, R., Hamlin, N., Hance, Z., Harper, D., Hauser, H., Horrsby, T., Holroyd, S., Kerhornou, A., Knights, A., Konfortov, B., Kyes, S., Larke, N., Lawson, D., Lennard, N., Line, A., Maddison, M., Mcclean, J., Mooney, P., Moule, S., Murphy, L., Oliver, K., Ormond, D., Frice, C., Quail, M.A., Rabbinowitsch, E., Rajandream, M.A., Rutter, S., Rutherford, K.M., Sanders, M., Simmonds, M., Seeger, K., Sharp, S., Smith, R., Squares, R., Whitehead, S., Woodward, J., Sulston, J.E., Craig, A., Newbold, C. and Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lawson, D., Bowman, S. and Barrell, B.
Direct Submission
Submitted (18-NOV-1998) P.falciparum Genome Sequencing Consortium,
The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tränslation="KnydsIQDLIKSIDFWITLKENIKNIDIPTFQKYLIEKYNKIIK
NEMDVCYVDIVGCIENEEFMKKNEHKCNGYLKSLKEKYEKNDINFEEECKYINENFI
EEIFTSDXSSPNLDIKNEKDISSDNKNKNKNNNNNNNNNNDDDFHNNNSYIQNND
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LSVEMFYRDNYFYFHCLNKYIKSKNKIEGLIICKLLTYLDLLRSYNTHGLNKTFQRLM
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                                                                                                                                                                                                                                                                Churcher, C., Harris, B., Harris, L.,
Moule,S., Mungall,K., Murphy,L., Oliver,K., Quail,M.A.,
Rajandream,M.-A., Rutter,S., Skelton,J., Squares,R., Squares,S.,
Sulston,J.E., Whitehead,S., Woodward,J.R., Newbold,C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CB10 15A, UK
On Apr 30, 2000 this sequence version replaced gi:4493924.
For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum.
Location/Qualifiers
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                                                                                                                  The complete nucleotide sequence of chromosome 3 of Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the orphan peptides from proteomics study (source: M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13 Nature 419 (6906), 527-531 (2002)
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/note="Possible exon as peptide fragment matches
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/protein id="CAD49086.1"
/db_xref="G1:3347694"
/db_xref="SPIREMBL:Q81222"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="MAL3P4.27"
/note="synonym: PFC0430w"
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Nature 400 (6744), 532-538 (1999)
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isolate="3D7"
db_xref="taxon:36329"
chromosome="3"
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                                                                                     Barrell, B.G.
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                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
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/translation="MKVGIIFFCLFFFVVLGACNNVKERIFKNIKKRTKFIILNEPIV
DLSFSBRLHFTLLEDLDVDRALYTLDESLANENLNYSSIFRLLVUTYKNIKENBDDN
KRIRY IFLGTSFSRIHPLNFEYFLRKLNKY YNGNIYERGNVDIRGILEEYNKEIEEK
KLEKQKLNKIKDKNNNNNNNSKFSKOGDNEDFNNKNDLYNFSDELYNNNDDIDVHB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLEBI ITKEKR PFLADDDDNDSNDKYILKTDEVNKYKGF FIGYGFNDDI PSVIHHYNF
DKNE HP PSLAGGI ILDI ITLIKNI YEVSHOLLLSONBENDG HIDY ITKEVYKY ITENLRV
BLITHSENVCLAKEQNIHLLDNDPNNFEI YKY YQVLANF KDYNKYTESKQY SKI GHENV
RHEETSSEGNENLARNITKHNDNNNDNNYSEDAIABLLLSYFNVFY PISTCNCYSIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HENLVTHKNILLGIKTSINTEEERIPHIKNTYDNKENTOIIFNTFNYDNKLKEKNTFG
FYNNSLLQNALENDNIDLDIIYMSDKESQKYDNLYFNSKVTSKEGLCEKLKHMIYYYY
EEYVMKNSEKKYFFIADDDTFVNVKNLIDVTNLTLNTCSHSKKYMYDKYIKSYDFVKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NBALFLQNFPKKTLFLYSYLKDTFAKTLQTLKKYDYVPKYCQGGILSKKHKINDSDDD
HDHHVGNKQNNDSTNHQDIEKNQVNVINNNNNNNKAKSIPIYEGRRYSYNTFSTNS
NEYFYDYLTGGAGILINDETAKRIYECKECTCPSTNSSMDDMIFGKWAKELGILAINF
EGYFQNSPLDYNKKYINTLVPITYHRLNKNRTTKESRDMYFNYLVNYNRNDKEQNKDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YUDYLDRNHKUMI DNVFHYFFYNMYDEKNKVYTKI EHRRINSKYNKSENDLAGAUN
GODKRYNDDENYNDDENYKGDENYKGDENYKGDEYMKGDENVKGDENVKDDENVKDDEN
NIKGDDNYNYDDRNHI DDI INMYEGYDDYMERNKGFTGKEKDDKAHNNEKATO
KKSSYPTNAI DRNEDTYRYDI YMYBESYDDYMERKEKDDKAHNNEKATO
KI KKKNEKAKKEKEKMOLKKOKDYTNNYFHYSOMOGREPYQQKMARYONGENEPYFG
KI KKKNEKAKKEKEKMOLKKOKDYTNNYFHYSOMOGREPYQQKMARYONGENEPNFF
DQREDELEDA I NPMDY BESYMENI, SNFEDDGEFYDEYDDFVNTI NADKLKI NDQNK
                                                                                                                                                                                                                                                             /note="Signal peptide predicted by SignalP 2.0 HMM (Signal peptide probabilty 0.995, signal anchor probability 0.005) with cleavage site probability 0.397 between residues 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKHESLMDYDKYHMINLENDIKLKHYIKETEBIHFNSIEBYKMKLNRINYKYDTLLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complement (7161. 13970)
/gene="MAL3P4.25"
/nocle="synonym: PFC0440c"
complement (7161. 13970)
/gene="MAL3P4.25" 13970]
/gene="Mal3P4.25" 13970]
/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKKY FNNSSSI KNTGNYYKNDNI DKSYDMCBRRSMMDRDENI YNNYKNKNRNNK
NYSNNI NHMDNRRNTYKGDLDGRKQYLSNKHYESKNDNENSYNLKKYNFNI PPI KYN
NNNNNNNNNNNNDRQNI DNNI YKFYDDKNEKKSNKTHSYGNNFNNEFNTFNDPKQNYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNESHNYTQDGHFTYNHNNNNDGRIXNKKDISLSSYGTNKISNDNLSKENTSYINQY
NNSGGANRHVINAQHNNNQHNNNQHNNFNYHNYKNAKPYPQDKYKNGDSFKFSAYNAE
QHDNNDKAYYQDHKNNMTHSTKGDTAISFNOGNYFGSFKNNKQMKERKFFKFRFRGS
SINRPGHNNNNNYYNNNNNNNYYNNHFCDDAERRNNKDNENGEILSYBLDGDAERNNNNNYYNNNNNNYYNNHFCDDAERRNNKDNENGEILSYBLDGDAERNNNNNYYNNNNNNYYNNNHFCDDAERRNNKDNENGEILSYBCDGD
MPIYNAANGNLKKAHTYRNDKKEKERKIKILLTEDNYNNNVQSNIEKLSIYKGRNEILEN
IEKNDYTFINGETGSGKSTCVPKFLLEENIRENKKINIIVTEPRRIACIALSKILSEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TNEKLGQKI CYRI SGESLYDSEKTVITYITICYLFKIFLHHYNNYKKFTHVI IDEIHD
RSILLDIVLLFIKLYLHNKQKDEQMFKLI IMSATMQSNLFYSYFEHPNI KMGSIFIGT
KIFSIDTFYIEDI INYTRYGSRNIHDEKINDEKINDEKINDEKINDEKINDDNKKSCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KNI BYNDKKKAHILUVKKWINKSSMBORKGRCGRTCHGICIRMI SKUFLNILLEDHKI SE
I YTHSILHLLYLY ILKSMSVLNGL INKRNEVVHCDNTNVYNVKBVKDOKNGICKNBISH
SHAENKKLTI YDVLSMI I BKPSKEKI KSTRYELEKVKAVIKI KDKLVI SI I GQIMIRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation="MNNTFKINKKRRTVYESYNIINIANKKRYMCNDNKMDNDNNIIN
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HRTDIKIHIHMLHSCLYDNTIHKLKHNDTDINIFLSSNIAESSITIPNVRLVIDFCIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FNNNNNKYCNDKNKDLDVDEIIPANVFSNISNLÇLELVYNLCLKGDSVIIFLSGMQDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HLYEQIKDIAQPPVNFQNDQNSNTFDFDTDEL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/product="hypothetical protein"
/protein_id="CAA15616.1"
/db_xref="G1:3764023"
/db_xref="SPTREMBL:077361"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
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/protain_id="CAA15615.1"
/db_xref="G1.3764022"
/db_xref="G0A:077360"
/db_xref="GOA:077360"
                                                                      'note="synonym: PFC0435w"
                                                                                                                                                                                                     gene="MAL3P4.26"
gene="MAL3P4.26"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and 18"
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TPLE I HGS PNLEDLNEGKKKSKKLANVLNPHI DNKLDVRUCTYFSGYTTPDINILK
RAIC (UMCPYLSPDI YVSKUI YYVY FEININNYTHNYTHNI LKGDDESYYRYTT CDRGAD.
NSVNS YLLI COPWIAL TOGGHDTDGITSF GVSPLANNNYTHNI LKGDDESYYRYTT CDRGAD.
NNSQNNYPMIKMINSNYSESET NLTSGRAY PDI I EKIRNKLLYKYNNNYEKSI FHNFY
NNI LAIL QOPWIAL VPVSNKYDEI INNAS I CTINI I NMFSNKT I FTMPL FNNNSLEKKCEV
SEN YHHYTELKKPKHLF LVWMPLLTDNYKIKKNKOKKHVETNITNALYNNNSLEKNYS
KND I HRDNI NDYSCHADGEDQYNKGYYYDDYDDYDDDDDDNUDDNNDNNNNNNDDNN
NNNDDDYLSNVKYKESDNNNTHQNNPDYSCHADGSSMCSDNNKKSKÇKKKCNLNFRSY
LGFL SMCPFHFDTRNI YDNQTADI YVGSLIDSYTNDTYTHWNYYTHDFNYSTITF
STI DYHDNY I CQFRYNLYTHYYNSDILSI I LKWMKKMKHKHKKNKTHYTDNY
STINNYTHNYTH YT TOTLLLSILLSILLSIN BONDDEN DEN TENSTERF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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/db_xref="GI:767213"
/db_xref="SPTREMBL:09NFE6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INKDGPNNDNRVDANDKAVNGNDKOVANDNDKAVNSQDNQGNQKOHFDDEDEEYFSDED
IMSDIEBNNIILKENLYLKQIVINMIEBNNMDYINYNKYSMDNMDIDEHFNLQYLYEDE
HFINLNEKWYNNKGEILMNTYDYLYNSLKNENDYNQYNNNNNNNNNNNSSYMYKNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="Revised: new gene prediction; splicing confirmed in
                      QXAYFDGNTYSEPIMLRNVFLEWLCYYLLYVQGLKKENKFHRKELKTYYMNTCSIMNK
RNHVNSKKLLCVINSVDNLCKKMLKMLNKNSNAYKSCYYLLYLLRGGSDINYNMGNNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IYIYELIKNQQYKKLMNCINNNIGNEYNNCDYSYLKNDKNFICNIRKYILNTISISFE
SIYLKNMSEYLNIQDNIQLEQFLNENKWTIKMINHKGKDEQICYNGNIETVQNKKNIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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NLSINLCRLLLYGVLLDVTFDTIILIGILNTNDIFPNINLYSSKNIYSYAVSLEICSK
                                                                                NNNNDNSGEIINADGITPNNTHMNEINGMNVFNVVTKYCLFDYSNQNIYLKFLFSLSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEKALNSLEAVKSSYLNNNFSVQVQNTMNAYERTNSEDFLFFQPINISPIKEANYKLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NDVMLTLLRIFCLYPHCYDKDIIKKILICVLYNINNVDMNMYMSLINSSLYDDNIKSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 AAAAUMNNNNMAUAUGUNNNNNNNCUNNNUUUNNNNNNAAAAANUANAAAACAUNNNNNCUU 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC099283 227182 bp DNA linear HTG 13-MAY.
Rattus norvegicus clone CH230-133B5, WORKING DRAFT SEQUENCE, 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.7%; Score 28.6; DB 3; Length 113880; 21.8%; Pred. No. 3.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="variable sequence, 9 or 10 Ts"
complement(join(16039. .16667,16813. .16891))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (join (16039. .16667, 16813.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC099283.6 GI:30579809
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             join(18192. .18242,18754. .19140)
/gene="MAL3P4.24"
/note="synonym: PFC0445w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMYYNEVAPILDKFRRTNROV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IYFTEDNIGSYITKLNH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="PFC0441c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene="PFC0441c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 227182)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 21.8
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 yoelii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         variation
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AC099283/c
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
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KEYWORDS
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Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrei,R., Calderon,B.,
Cardenas,V. Carter,K., Cavazos,I., Casaar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., Diyacus,I.
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., Diyacus,I.,
Davils,M.L., Davis,C., Davy-Carroll,L.,De Anda,C., Dederich,D.,
Began,A., Beochco,M., Spenson,S., Dunn,A., Dural,B., Eaves,K.,
Frasscr,C.M., Gabls,A., Galls,M., Garcia,A., Garner,T., Garza,M.,
Gubrarde,S., Finley,M., Flagy,N., Porbes,L., Foster,M., Foster,P.,
Frasscr,C.M., Gabls,A., Galls,R., Garner,T., Garza,M.,
Gurarde,S., Finley,M., Flagy,N., Porbes,L., Foster,M., Gusvara,M.,
Harvey,Y., Havlak,P., Hawdes,A., Henderson,N., Hamilton,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Hawdes,A., Henderson,N., Idlebrad,D., Joster,P.,
Jackson,J., Jacop,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
Karpethy,S., Kally,S., Relly,S., Khaly,Z., Khan,L., Knag,L., Li,Z., Liu,J.,
Liu,J., Liu,M., Liu,Y., Lobow,H., Levan,J., Manlo,M., Manlo,M.,
Mangum,B., Mapua,P., Martin,K., Martin,R., Ma,J.,
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Plopper,P., Poinder,P., Popovic,D., Primus,B., Phi,L.,
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Plopper,P., Poinder,A., Popovic,D., Primus,B., Phi,R., Raylor,C.,
Ravelly,M., Shart,H., Royas,A., Roster,M., Tablor,P., Raylor,C.,
Sands,A., Sharten,A., Watch,N., Sheet,M., Tablor,P., Taylor,C.,
Taylor, C., Nodey,T., Rojas,A., Soctet,A., Tablor,P., Taylor,C.,
Taylor, Williams,G., Warren,J., Watch,S., Yen,J., Yoon,U., Yoon,U.,
Walas,R., Watch,R., Sharten,B., Sheet,M., Sharten,R., Walas,R., Watch,R., Sharten,R., Walas,R., Sheet,M., Sharten,R., Walas,R., Sheet,M., Sharten,R., Walas,R., Sheet,M., Sharten,R., S Direct Submission
Submitted (13-MAY-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On May 13, 2003 this sequence version replaced gi:25086297.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature Submitted (09-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 227182)
Rat Genome Sequencing Consortium. (bases 1 to 227182) Worley, K.C. Direct Submission

AUTHORS TITLE JOURNAL

TITLE JOURNAL REFERENCE

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REFERENCE AUTHORS TITLE JOURNAL

COMMENT

-- Genome Center

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* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft" sequence. It currently

* consists of 3 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N. but the exact sizes of the gaps are unknown.

* This record will be undated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                  Center project name: GKCS
Center clone name: GKC3
Center clone name: Statistics
Consensus quality: 221120 bases at least Q40
Center guality: 223333 bases at least Q30
Center guality: 223333 bases at least Q20
Estimated insert size: 228594; sum-of-centigs estimation
Quality coverage: 9x in Q20 bases; sum-of-centigs estimation
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Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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/note="wgs end_extension clone end:Sp6" |
1284.3927 /note="wgs end extension clone_end:Sp6" |
5122. .5977 /note="clone_boundary clone end:Sp6 site:EcoR1
                                                                                                                ---- Project Information
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0; Gaps 26.7%; Score 28.6; DB 2; Length 227182; 21.8%; Pred. No. 2.6e+02; Live 12; Mismatches 67; Indels 0; Query Match Best Local Similarity 21.8% Matches 22, Conservative ≽

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109383 TAGACAGTCATAGAAAATAAAGGACTCAAAAAAAACTCTTA 109343 

earch completed: March 8, 2004, 05:20:24 ob time: 2071 secs

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This invention describes novel copper-containing ribonucleoproteins which are ternary complexes of an $100 protein, copper ions, and RNA comprising the following consensus sequence or its complement GGAAAAUNNUNDARGAIGNIGCUNNNUUUNNNNNNAAAAANO-LTANAAACANO-SCUNNACHO-33AGAA-AUNO-16UUAGCAS where N = G, A, U or C. The ribonucleoproteins are stated to have the following properties (1) cell-selective morphogenic action in vitro on isolated primary and/or cloned blood capillary endothelial cells in culture for the non-mitogenic induction of the change in cell phenotype from the
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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ABL18738
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4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	RESULT 1 AAX23773  AAX23773  AAX23773;  AAX21999 (fir:AXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                 insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAAAAUNNNNNAUAUGNNNNNNCUNNNNUUUNNNNNAAAAANUANAAACAUNNNNC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 3456;
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                                                                                                                                                                                                                                             utuguacauaaaaauaaaacaugacuucuuuagacacuccuucauuagaaauaaaauaa 148
                                                                                                                                                                                                                      91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 AAAAUNNNNNNNAUAUGMNNNNNCUNNNNUUUNNNNNAAAAANUANAAAACAUMNNNNCUU 62
confluent state, for non-mitogenic alteration of the spatiotemporal supracellular organisation of cells into three-dimensional organoid, capillary-like structures in culture, (2) a specific chemotropic action on blood vessels in vivo, (3) induction of directional growth of blood vessels in vivo and (4) induction of neovascularisation of tissues through directed ingrowth of blood vessels. Their use for modulating
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      developmental biology; cell signalling; insecticide;
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                                                                                                                                                       Length 298;
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                                                                                                                                                                                    44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                         Sequence 298 BP; 103 A; 40 C; 38 G; 0 T; 117 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .69
                                                                                                                                                     29.3%; Score 31.4; DB 2; 42.1%; Pred. No. 6.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 29.4; DB 2;
                                                                                                                                                                                    Mismatches
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10; Mismatches
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210000
310000
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710000
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                                                                                                                                                                                                                                                                                                        149 AAUAAACUAÜÜÄGCÄG 164
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500001
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1300001
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                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pharmaceutical; gene; ds
                                                                                         angiogenesis is claimed
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                                                                                                                                                                                                                                                                                                                                                RESULT 2
AAV21209 05/c
Continuation (6 of 17) of
WP Sequence split into 17
WP Fragment Name
                                                                                                                                                                     Local Similarity
nes 32; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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AAV21209 01
AAV21209 02
AAV21209 04
AAV21209 04
AAV21209 06
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AAV21209 06
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AAV21209 07
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AAV21209_12
AAV21209_13
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AAV21209_15
AAV21209_16
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Matches
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RESULT 3 ABL18738

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Gaps

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Myers

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and insecticides. Interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL0404L16175) and the encoded proteins (ABBS7737-ABR30222). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4829 BP; 1251 A; 1183 C; 1154 G; 1241 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 7663; 21pp + Sequence Listing; English.
PWD,
    ŗ
    Adams M,
                                                                                        WPI; 2001-656860/75
         Venter
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DB 4; Length 4829; Indels 36; 13; Mismatches 27.3%; Score 29.2; 25.0%; Pred. No. 36 Conservative Query Match Best Local Similarity 21;

. 0

Gaps

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|||||||: 3811 GGAAAATAAACTIAGTAITIACAAICTIAGTITITGIACCAAAAAATAAAAATCIGTAIAA 3870 GGAAAAUNNNNTUNAUAUGNNNNNNCUNNNNUUUNNNNNNAAAAANUANAAACAUNNNNNC 60 व ≿

:: | | | | : 3871 ITAAATTCAAATTTAAAT 3894 UUNAGNNNNNNNNNNNAGAAAU 84 61

ABQ89024 standard; cDNA; 524 BP ABQ89024

ESULT 5

ABQ89024;

(first entry) 27-SEP-2002

Human prostate expressed polynucleotide SEQ ID NO 280.

Human; prostate; cytostatic; tumour; cancer; vaccine; gene therapy; gene;

Homo sapiens

WO200255700-A2

18-JUL-2002.

07-DEC-2001; 2001WO-US047349.

07-DEC-2000; 2000US-0254648P. 13-MAR-2001; 2001US-0275688P.

(CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.

Kita D; Ď, Leshkowitz ), Kaasam A, Lamson G, Drmanac R; on M, Drmanac S, Labat I, Leshkowi Stache-Crain B, Scott EM; Garcia PD, Ka R, Dickson M, Jones WL, Escobedo J, Ga Crkvenjakov R, Garcia V,

WPI; 2002-557824/59

New genes and gene products isolated from human prostate, useful for treating or diagnosing tumor or cancer (e.g. prostate cancer or breast cancer), or as vaccines for treating or preventing these diseases.

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Complement. The polynucleotides and gene products are useful for treating or diagnosing tumour or cancer (e.g. prostate cancer, breast cancer, lung cancer or medullary carcinoma) in a subject (e.g. cattle, dogs, cats, rabbits, horse or human). The polynucleotides and polypeptides are also polynucleotides and polypeptides are also polynucleotides are useful for gene therapy. The present sequence is that off one of a group of polynucleotides (AsQ88745-AB20015) disclosed electronically as sequences of the invention. However only 1271 polynucleotides are given, whereas 1477 polynucleotides and 91 proteins are claimed. Note: The sequence this peacent did not proteins are claimed. Note: The sequence character of this peacent did not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                   form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequence
                                                                      invention relates to an isolated polynucleotide comprising any of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GAAAAUNNNNNUAUAUGINNNNNNCUNNNNUUUNNNNNAAAAANUANAAAACAUNNNNNNCU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 GAAAACTCTTGTTAGACATGATGTTTCCTATACAGAAGAAAAGATACAAACTTGATTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6; Length 524;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 524 BP; 132 A; 107 C; 110 G; 159 T; 0 U; 16 Other;
                    Claim 1; SEQ ID NO 280; 186pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               292 TCAGTAAAAACACTTTTAGAGATTGTGTTTTCCTTTTTTGTGAG 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Mismatches
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Human cDNA sequence useful for the treatment of cancer (SeqID 280). ВЪ ADB81968 standard; cDNA; 524 (first entry) 04-DEC-2003 ADB81968; ADB81968 

RESULT 6

Homo sapiens.

human; prostate; cancer; cytostatic; gene therapy; vaccine;

response; gene; ss.

immune

WO2003050236-A2

19-JUN-2003.

04-SEP-2002; 2002WO-US028214.

07-DEC-2001; 2001US-00012697.

(CHIR ) CHIRON CORP (HYSE-) HYSEQ INC.

à Kita Leshkowitz D, Kassam A, Lamson G, Drmanac R; I, Drmanac S, Labat I, Leshkow Scott EM; Stache-Crain B, Dickson M, Garcia PD, Jones LW, Escobedo J, Ga Crkvenjakov R, García V,

WPI; 2003-513972/48.

New polynucleotides derived from human prostate, useful for modulating immune response to prevent or treat cancer.

ID NO 280; 188pp; English. Claim 1; SEQ

This invention relates to novel isolated polynucleotides of human origin, particularly isolated from the human prostate. Specifically, it refers to the diagnostics and therapeutics comprising these novel human

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polynucleotides, and includes the derived probes, antisense oligonucleotides and antibodies thereof. The identification of these human prostate genes that can inhibit tumour growth is useful for understanding the progression and nature of complex diseases such as cancer, and hence they are important in the drug discovery process. The present invention describes these polynucleotides and encoded polypeptides as exhibiting cytostatic activity, and through gene therapy and/ or vaccines they can be used to modulate the immune response for the prevention or treatment of cancers, particularly of the prostate, but also for breast, lung and colon cancer. This polynucleotide sequence is a human cDNA sequence useful for the treatment of cancer, used in an exemplification of the invention. NOTE: These sequences are not given in the specification but are provided on the WIPO website.
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Sequence 524 BP; 132 A; 107 C; 110 G; 159 T; 0 U; 16 Other;

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                                                                                                                              2 GAAAAUNNNNNHUAUAUGNNNNNCUNNNUUUNNNNNAAAAANUANAAACAUNNNNCU 61
                                          Gaps
                                             ·,
Query Match 25.6%; Score 27.4; DB 8; Length 524; Best Local Similarity 24.3%; Pred. No. 87; Matches 25; Conservative 9; Mismatches 69; Indels (
                                                                                                                                                                       292 TCAGTAAAACACTTTTAGAGATTGTGTTTTCCTTTTTTGTGAG 334
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ADB82181 standard; cDNA; 761 BP. (first entry) 04-DEC-2003 ADB82181; ADB82181 RESULT

Human cDNA sequence useful for the treatment of cancer (SeqID 493).

human; prostate; cancer; cytostatic; gene therapy; vaccine; gene; ss response; immune

Homo sapiens.

WO2003050236-A2

19-JUN-2003

04-SEP-2002; 2002WO-US028214

07-DEC-2001; 2001US-00012697

(CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.

Kita D;

Garcia PD, Kassam A, Lamson G, Drmanac R; R, Dickson M, Drmanac S, Labat I, Leshkowitz D, ones LW, Stache-Crain B, Scott EM;

Jones LW,

Garcia V,

Crkvenjakov R,

Escobedo J,

New polynucleotides derived from human prostate, useful for modulating immune response to prevent or treat cancer. WPI; 2003-513972/48

Claim 1; SEQ ID NO 493; 188pp; English.

This invention relates to novel isolated polynucleotides of human origin, particularly isolated from the human prostate. Specifically, it refers to the diagnostics and therapeutics comprising these novel human polynucleotides, and includes the derived probes, antisense oligonucleotides and antibodies thereof. The identification of these human prostate genes that can inhibit tumour growth is useful for understanding the progression and nature of complex diseases such as

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated polynucleotide comprising any of 1477 sequences or its fragment, degenerate variant, antisense or complement. The polynucleotides and gene products are useful for treating or diagnosing tumour or cancer (e.g. prostate cancer, breast cancer, lung cancer or medullary carcinoma) in a subject (e.g. cattle, dogs, cats, rabbits, horse or human). The polynucleotides and polypeptides are also useful as vaccines for treating or preventing these diseases. The polynucleotides are useful for gene therapy. The present sequence is that of one of a group of polynucleotides (ABQB8745-ABQ90015) disclosed
cancer, and hence they are important in the drug discovery process. The present invention describes these polynucleotides and encoded polypeptides as exhibiting cytostatic activity, and through gene therapy and/ or vaccines they can be used to modilate the immune response for the prevention or treatment of cancers, particularly of the prostate, but also for breast, lung and colon cancer. This polynucleotide sequence is a human cDNA sequence useful for the treatment of cancer, used in an exemplification of the invention. NOTE: These sequences are not given in
                                                                                                                                                                                                                                                                                                                                Human; prostate; cytostatic; tumour; cancer; vaccine; gene therapy; gene;
                                                                                                                                                                                                                                                                                                       2 GAAAAUNNINNINAUAUAUGINNINNINNINUUUNINNINNINAAAAANUANAAACAUNINNINCU 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New genes and gene products isolated from human prostate, useful for treating or diagnosing tumor or cancer (e.g. prostate cancer or breast cancer), or as vaccines for treating or preventing these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drmanac R;
, Leshkowitz D,
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                                                                                                                                                                                                                             25.6%; Score 27.4; DB 8; Length 761;
                                                                                                                                                                                            Sequence 761 BP; 197 A; 167 C; 168 G; 214 T; 0 U; 15 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 419; 186pp + Sequence Listing; English
                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                   297 TCAGTAAAACACTTTTAGAGATTGTGTTTTCCTTTTTTGTGAG 339
                                                                                                                                                     the specification but are provided on the WIPO website.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human prostate expressed polynucleotide SEQ ID NO 419.
                                                                                                                                                                                                                                                                      69;
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on M, Drmanac S, Labat I,
Stache-Crain B, Scott EM;
                                                                                                                                                                                                                                                                      9; Mismatches
                                                                                                                                                                                                                                                    Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABQ89163 standard; cDNA; 769 BP
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                                                                                                                                                                                                                                                    24.3%;
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R, Dickson M,
                                                                                                                                                                                                                                                                    25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escobedo J, Gar
Crkvenjakov R,
Garcia V, Jones
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                                                                                                                                                                                                                                   Query Match
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us-09-646-651c-2.rng

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electronically as sequences of the invention. However only 1271 polynucleotide sequences are given, whereas 1477 polynucleotides and 91 proteins are claimed. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequence

Sequence 769 BP; 179 A; 185 C; 196 G; 169 T; 0 U; 40 Other;

2 GAAAAUNNNNUNAUAUGNNNNNNCUNNNNUUUNNNNNAAAAANUANAAAACAUNNNNNCU 61 Gaps 0; Query Match 25.6%; Score 27.4; DB 6; Length 769; Best Local Similarity 24.3%; Pred. No. 91; Matches 25; Conservative 9; Mismatches 69; Indels ( አ 9

0;

148 TCAGTAAAAACACTTTTAGAGATTGTGTTTTCCTTTTTTGTGAG 190

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RESULT

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ADB82106 standard; cDNA; 769 BP ADB82106;

(first entry) 04-DEC-2003

Human cDNA sequence useful for the treatment of cancer (SeqID 418).

human; prostate; cancer; cytostatic; gene therapy; vaccine

immune response; gene; ss.

Homo sapiens

WO2003050236-A2

L9-JUN-2003

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04-SEP-2002; 2002WO-US028214.

07-DEC-2001; 2001US-00012697.

(CHIR ) CHIRON COR (HYSE-) HYSEQ INC.

Leshkowitz D, Kita D; Garcia PD, Kassam A, Lamson G, Drmanac R; R, Dickson M, Drmanac S, Labat I, Leshkow: ones LW, Stache-Crain B, Scott EM; Jones LW, Stache-Crain B, Crkvenjakov R, Escobedo J, Garcia V,

WPI; 2003-513972/48.

New polynucleotides derived from human prostate, useful for modulating immune response to prevent or treat cancer.

Claim 1; SEQ ID NO 418; 188pp; English.

This invention relates to novel isolated polynucleotides of human origin, particularly isolated from the human prostate. Specifically, it refers to the diagnostics and therapeutics comprising these novel human polynucleotides, and includes the derived probes, antisense oligonucleotides and antibodies thereof. The identification of these human prostate genes that can inhibit tumour growth is useful for understanding the progression and nature of complex diseases such as cancer, and hence they are important in the drug discovery process. The present invention describes these polynucleotides and encoded polypeptides as exhibiting cytostatic activity, and through gene therapy and/or vaccines they can be used to modulate the immune response for the prevention or treatment of cancers, particularly of the prostate, but also for breast, lung and colon cancer. This polynucleotide sequence is a human cDNA sequence useful for the treatment of cancer, used in an exemplification of the invention. NOTE: These sequences are not given in

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                                                                       769;
                                    Sequence 769 BP; 179 A; 185 C; 196 G; 169 T; 0 U; 40 Other;
                                                                                                         Indels
                                                                                                                                                                                                                148 TCAGTAAAAACACTTTTAGAGATTGTGTTTCCTTTTTTGTGAG 190
the specification but are provided on the WIPO website.
                                                                 Query Match 25.6%; Score 27.4; DB 8; Best Local Similarity 24.3%; Pred. No. 91; Matches 25; Conservative 9; Mismatches 69;
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BP ABQ89160 standard; cDNA; 789 RESULT 10 ABQ89160

AB089160;

(first entry) 27-SEP-2002 Human prostate expressed polynucleotide SEQ ID NO 416

Human; prostate; cytostatic; tumour; cancer; vaccine; gene therapy; gene;

Homo sapiens

WO200255700-A2

18-JUL-2002

07-DEC-2001; 2001WO-US047349.

07-DEC-2000; 2000US-0254648P. 13-MAR-2001; 2001US-0275688P.

(CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.

Kita Kassam A, Lamson G, Drmanac R; 4, Drmanac S, Labat I, Leshkowitz D, ache-Crain B, Scott EM; Stache-Crain B, Crkvenjakov R, Dickson M, Garcia PD, Garcia V, Jones WL, Escobedo J, 

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WPI; 2002-557824/59.

New genes and gene products isolated from human prostate, useful for treating or diagnosing tumor or cancer (e.g. prostate cancer or breast cancer), or as vaccines for treating or preventing these diseases.

Claim 1; SEQ ID NO 416; 186pp + Sequence Listing; English.

The invention relates to an isolated polynucleotide comprising any of 1477 sequences or its fragment, degenerate variant, antisense or complement. The polynucleotides and gene products are useful for treating or diagnosing tumour or cancer (e.g. prostete cancer, breast cancer, lung cancer or medullary carcinoma) in a subject (e.g. cattle, dogs, cats, rabbits, horse or human). The polynucleotides and polypeptides are also useful as vaccines for treating or preventing these diseases. The polynucleotides are useful for gene therapy. The present sequence is that of one of a group of polynucleotides (HADO8745-ABQ90015) disclosed electronically as sequences of the invention. However only 1271 polynucleotide sequences are given, whereas 1477 polynucleotides and 91 profess are claimed. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequence

Sequence 789 BP; 199 A; 185 C; 186 G; 181 T; 0 U; 38 Other;

61

2 GAAAAUNNNNNNAUAUGUNNNNNNNNNNUUUNNNNNAAAAANUANAAAACAUNNNNNNCU

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                                                                                                                                                                        This invention relates to novel isolated polymuclectides of human origin, particularly isolated from the human prostate. Specifically, it refers to the diagnostics and therapeutics comprising these novel human polymucleotides, and includes the derived probes, antiesnse oligonucleotides and antibodies thereof. The identification of these human prostate genes that can inhibit tumour growth is useful for understanding the progression and nature of complex diseases such as cancer, and hence they are important in the drug discovery process. The present invention describes these polymucleotides and encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptides as exhibiting cytostatic activity, and through gene therapy and or vaccines they can be used to modulate the immune response for the prevention or treatment of cancers, particularly of the prostate, but also for breast, lung and colon cancer. This polymucleotide sequence is a human cDNA sequence useful for the treatment of cancer, used in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exemplification of the invention. NOTE: These sequences are not given in
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                                                                                                                         2 GAAAAUNNNNUNAUAUGUNNNNNNCUNNNUUUNNNNNAAAAAUUANAAAACAUNNNNNCU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotides derived from human prostate, useful for modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kita
                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human cDNA sequence useful for the treatment of cancer (SeqID 415).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escobedo J, Garcia PD, Kassam A, Lamson G, Drmanac R;
Crkvenjakov R, Dickson M, Drmanac S, Labat I, Leshkowitz D,
Garcia V, Jones LW, Stache-Crain B, Scott EM;
                                                                                ;
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               Length 789;
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25.6%; Score 27.4; DB 8; Length 789;
Best Local Similarity 24.3%; Pred. No. 91;
Matches 25; Conservative 9; Mismatches 69; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human; prostate; cancer; cytostatic; gene therapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 789 BP; 199 A; 185 C; 186 G; 181 T; 0 U; 38 Other;
                                                                       69; Indels
                                                                                                                                                                                                                                               62 UNAGNINININININININAGAAUNINININININININININININININININI
                                                                                                                                                                                                                                                                                                       157 TCAGTAAAAACACTITIAGAGATIGIGITICCITITITIGIGAG 199
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            Score 27.4; DB 6;
Pred. No. 91;
                                                                       9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immune response to prevent or treat cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 415; 188pp; English.
         25.6%;
24.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADB82103 standard; cDNA; 789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-DEC-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene; ss
                                                              25; Conservative
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immune response;
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                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
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The invention relates to an isolated polynucleotide comprising any of 1477 sequences or its fragment, degenerate variant, antisense or complement. The polynucleotides and gene products are useful for treating or diagnosing tumour or cancer (e.g. prostate cancer, breast cancer, lung cancer or medullary carcinoma) in a subject (e.g. cattle, dogs, cats, rabbits, horse or human). The polynucleotides and polypeptides are also useful as vaccines for treating or preventing these diseases. The polynucleotides are useful for gene therapy. The present sequence is that of one of a group of polynucleotides (ABQB8745-ABQ90015) disclosed electronically as sequences of the invention. However only 1271 polynucleotide sequences are given, whereas 1477 polynucleotides and 91 proteins are claimed. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequence
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                                                                                                                                                                                                                                                                                                     Human; prostate; cytostatic; tumour; cancer; vaccine; gene therapy; gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New genes and gene products isolated from human prostate, useful for treating or diagnosing tumor or cancer (e.g. prostate cancer or breast cancer), or as vaccines for treating or preventing these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 GAAAAUNNNNNAUAUGUNNNNNNNNUUUNNNNNNAAAAANUANAAACAUNNNNNCU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 494; 186pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lamson G, Drmanac R;
                                                                 157 TCAGTAAAACACTITITAGAGAITGIGITITCCTITITITGIGAG 199
                                      69; Indels
                                                                                                                                                                                                                                                                    Human prostate expressed polynucleotide SEQ ID NO 494.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escobedo J, Garcia PD, Kassam A, Lamson G, Dr
Crkvenjakov R, Dickson M, Drmanac S, Labat I,
Garcia V, Jones WL, Stache-Crain B, Scott EM;
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Best Local Similarity 24.3%; Pred. No. 92;
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                                                                                                                                                               ABQ89238 standard; cDNA; 835
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                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-557824/59
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                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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Gaps

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371 TCAGTAAAAACACTTTTAGAGATTGTGTTTTCCTTTTTTGTGAG 413
62
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ESULT 13 DB83094

ADB83094 standard; cDNA; 929 BP

(first entry) 04-DEC-2003

Human cDNA sequence useful for the treatment of cancer (SeqID 1307)

human; prostate; cancer; cytostatic; gene therapy; vaccine; immune response; gene; ss.

Homo sapiens.

WO2003050236-A2

19-JUN-2003.

04-SEP-2002; 2002WO-US028214.

07-DEC-2001; 2001US-00012697.

CHIRON CORP HYSEQ INC. (CHIR ) (HYSE-) H

Kita Labat I, Leshkowitz D, Garcia PD, Kassam A, Lamson G, Drmanac R; R, Dickson M, Drmanac S, Labat I, Leshkow. ones LW, Stache-Crain B, Scott EM; Jones LW, Crkvenjakov R, Garcia V, Jone Escobedo J,

WPI; 2003-513972/48.

New polynucleotides derived from human prostate, useful for modulating immune response to prevent or treat cancer.

Claim 1; SEQ ID NO 1307; 188pp; English.

origin, efers to prevention or treatment of cancers, particularly of the prostate, but also for breast, lung and colon cancer. This polynucleotide sequence is a human cDNA sequence useful for the treatment of cancer, used in an exemplification of the invention. NOTE: These sequences are not given in This invention relates to novel isolated polynucleotides of human origin, particularly isolated from the human prostate. Specifically, it refers to the diagnostics and therapeutics comprising these novel human polynucleotides, and includes the derived probes, antisense oligonucleotides and antibodies thereof. The identification of these human prostate genes that can inhibit tumour growth is useful for understanding the progression and nature of complex diseases such as cancer, and hence they are important in the drug discovery process. The present invention describes these polynucleotides and encoded polypeptides as exhibiting cytostatic activity, and through gene therapy and/or vaccines they can be used to modulate the immune response for the the specification but are provided on the WIPO website.

Sequence 929 BP; 243 A; 207 C; 211 G; 244 T; 0 U; 24 Other;

0; Gaps Score 27.4; DB 8; Length 929; Pred. No. 93; 9; Mismatches 69; Indels ch 25.6%; l Similarity 24.3%; 25; Conservative 3 Query Match Best Local Similarity Matches 25; Conserv

0;

297 TCAGTAAAACACTTTTAGAGATTGTGTTTTCCTTTTTTGTGAG 339

autoimmune disease; systemic lupus erythematosus; arthritis; rheumatism; osteoarthritis; osteoporosis; breast cancer; endometrial cancer. Human; Oestrogen receptor beta; ERbeta; ds; SNP; chromosome single nucleotide polymorphism; cardiovascular disease; Human Oestrogen receptor beta gene. AAS43104 standard; DNA; 325791 BP (first entry) 18-DEC-2001 AAS43104; AAS43104 

Homo sapiens.

WO200162793-A2

30-AUG-2001.

20-FEB-2001; 2001WO-US005360.

22-FEB-2000; 2000US-0183755P. 24-JAN-2001; 2001US-00768185.

(PEKE ) PE CORP NY

Winn-Deen ES; Hwang SS, Cassel MJ, Kalush F,

WPI; 2001-582041/65. P-PSDB; AAU27322 Estrogen receptor gene and protein polymorphisms useful for diagnosis of individuals at risk of developing bone disorders.

Example 2; Fig 1; 245pp; English.

The invention relates to a novel isolated peptide comprising or consisting of an amino acid sequence selected from an amino acid sequence consisting of an amino acid sequence selected from an amino acid sequence of a variant osstrogen receptor protein (e.g. RBbeta), or a fragment of 10 amino acids), antibodies against them, inclaic acids encoding them clocated on chromosome 67.25.1. The variant seem coded by single nuclectide polymorphisms (SNP). The variant peptides and proteins can be used in assays to determine the biological activity of the protein, to used in assays to determine the biological activity of the protein, to determine levels of the protein in biological fluids, to identify compounds that modulate receptor activity and to screen compounds for the ability to stimulate or inhibit interaction between the receptor protein and a target molecule that normally interacts with the receptor protein e.g. osetrogen. The antibody can be used to isolate the protein, to assess expression in disease states e.g. cardiovascular disease and autoimmune disease (e.g. systemic lupus erythematosus, arthritis, rheumatism and oslecarthritis), osteoporosis, breast cancer and endometrial cancer. In addition the antibodies can be used in pharmacogenomic analysis and inhibiting protein function, e.g. blocking the binding of the oestrogen receptor protein to a binding partner such as a ligand. The nucleic acide encoding the proteins can be used as probes, primers, chemical intermediates and in biological assays. The present sequence is the human Erbeta gene

Sequence 325791 BP; 94098 A; 68292 C; 67970 G; 95431 T; 0 U; 0

Gaps ô 25.2%; Score 27; DB 4; Length 325791; 20.8%; Pred. No. 2.5e+02; ive 12; Mismatches 68; Indels 0 Conservative Query Match Best Local Similarity Trines 21; Conservat

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205486 AAITTGACCTGCATATGCATACTCTATCTTTGGAAGAAAATACAACAAACTTGTAACATT 205545 3 AAAAUNNNNNAUAUAUGINNNNNNCUNNNNUUUNNNNNAAAAANUANAAACAUNNNNNCUU 62 à 임

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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AlDS, epilepsy, neurofibromatcsis, rheumatcoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antinfeumatic, antiarthritic, antidiabetic, antipsoriatic, antinflammatory, cancer, eye disease, arteriosclerosis, anaemia, acute myeloid leukaemia, Alzheimer's disease, AIDS; epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis, bowel disease, gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  system disease; cytosine methylation; antiasthmatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiarteriosclerotic, antianaemic, cytostatic, nootropic, neuroprotective, anti-HIV, anticonvulsant, ophthalmological,
205546 GATTGCTTCTGTGGAGAGGAACTGATAAGAGAAAATTTTA 205586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 239; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                            Human immune system associated gene SEQ ID NO: 239.
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                                                                                                                                                                           ABL32266 standard; DNA; 6419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JUL-2001; 2001WO-EP007537.
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Best Local Similarity 24.0
Matches 25; Conservative
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ABL32266/c
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1212 AAAAAACAACCTACCCAAAAATCACCCAACAAACTATTCTAACA 1169

Search completed: March 8, 2004, 04:45:33

Job time : 310 secs

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Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 13988, A
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Sequence 75, App
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Sequence 642, App
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3089, Ap
25, Appl
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Seguence 61, Appl
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Sequence 1, A
Sequence 3089
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-842-306B-5
US-08-842-306B-5
US-08-771-212A-5
US-09-621-976-1398
US-09-643-597-126
US-09-643-597-126
US-09-606-421B-126
US-09-601-198-75
US-09-601-198-75
US-09-601-198-75
US-09-401-064-281
US-09-401-064-281
US-10-204-708-32
US-09-596-002-31
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US-09-103-509-5
US-09-102-644-5
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Maximum Match 100%
Listing first 45 summaries
                                                      - nucleic search, using sw model
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Match Length DB
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Sequence 5, Appli Sequence 12, Appli Sequence 8, Appli Sequence 8, Appli Sequence 35, Appli Sequence 1, Appli Sequence 14, Appli Sequence 49, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 35, Appli Sequence 35, Appli Sequence 35, Appli Sequence 35, Appli Sequence 355, Appli Sequence 355, Appli Sequence 355, Appli Sequence 355, Appli Sequence 355, Appli	Methanogenic Archaeon, M
US-09-218-032-5 US-09-636-389-8 US-08-103-509-8 US-09-103-509-8 US-09-102-644-8 US-09-102-644-8 US-09-102-644-8 US-08-218-032-8 US-08-916-421B-1 US-08-916-421B-1 US-08-99-268-49 US-08-307-499-49 US-08-298-687A-6 US-08-298-687A-6 US-08-298-687A-6 US-08-298-687A-6 US-08-298-687A-6 US-08-298-687A-6 US-08-298-687A-6 US-08-543-681A-3553 US-08-543-681A-3553 US-10-204-708-94	LIGNMENTS  B Sequence of the 4,428  c, or g
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OTHER INFORMATION: n equals a, NAME/KEY: misc\_feature LOCATION: (312837). (312837)
OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
LOCATION: (312993)..(312993)
OTHER INFORMATION: n equals a, OTHER INFORMATION: (319226)
LOCATION: (319226)...(319226)
OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (234187) ..(234187) OTHER INFORMATION: n equals a, LOCATION: (191995)..(191995) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (231980)..(231980) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (674435)..(674435) OTHER INFORMATION: n equals a, LOCATION: (163385)..(163385) OTHER INFORMATION: n equals a, INFORMATION: n equals a, COCATION: (309398)..(309398) LOCATION: (309418)..(309418) OTHER INFORMATION: n equals a, LOCATION: (559167)..(559167)

OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (600992)..(600992) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (622708)..(622708) OTHER INFORMATION: n equals a, LOCATION: (713652)..(713652) OTHER INFORMATION: n equals a, OTHER INFORMATION: n equals a, OTHER INFORMATION: n equals a, NAME/KEY: misc\_feature LOCATION: (657081)..(657081) OTHER INFORMATION: n equals a, COCATION: (657203)..(657203) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (682442)..(682442) OTHER INFORMATION: n equals a, KEY: misc feature ION: (103998)..(103998) INFORMATION: n equals NAME/KEY: misc feature LOCATION: (234814)..(234814) (234220)..(234220) NAME/KEY: misc feature LOCATION: (559241)..(559241) NAME/KEY: misc feature LOCATION: (163385)..(16 feature WAME/KEY: misc\_feature NAME/KEY: misc feature LOCATION: (309398)..(30 NAME/KEY: misc feature LOCATION: (309418)..(30 NAME/KEY: misc feature LOCATION: (559167)..(55 NAME/KEY: misc\_feature NAME/KEY: misc\_feature NAME/KEY: misc COCATION:

573299 AAAATTAGTATTAGAAGCTATAACTTATTTAATGCCAAAAAATATAAACATTTCTGGTG 573240 3 AAAAUNNININININININAUAUGINININININININININININININAAAAANUANAAAACAUNINININIOU 62 Length 1664976; . 0 573239 AATAATGACAGGCAAAGTTATCTTAGTAGGAGCAGGACCGGGAG 573195 69; Indels DB 4; Mismatches Query Match 27.5%; Score 29.4; Best Local Similarity, 24.8%; Pred. No. 4; б b orÖK ΟĽ ö or g or or oχ or or or ö οχ or or ÖK ΰ ΰ Ö ϋ ΰ ΰ ; Sequence 642, Application US/09328352 ; Patent No. 6562958 LOCATION: (1096846). (1096846)
OTHER INFORMATION: n equals a, t.
NAME/KEY: misc\_feature
LOCATION: (1119881). (1119881)
OTHER INFORMATION: n equals a, t.
NAME/KEY: misc\_feature
LOCATION: (1130881). (113081)
OTHER INFORMATION: n equals a, t. 10; OTHER INFORMALL...
NAME/KEY: misc feature
LOCATION: (1084830)
OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (779455)..(779455) OTHER INFORMATION: n equals a, LOCATION: (779676)...(779676)
OTHER INFORMATION: n equals a,
NAME/KEY: misc feature.
LOCATION: (855539)...(855539)
OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (871619) ..(871619) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (1310988)..(1310988) OTHER INFORMATION: n equals a, NAME/KEY: misc\_feature; ! LOCATION: (1664954)..(1664855) OTHER INFORMATION: n equals a, US-08-916-4218-1 LOCATION: (1313224)..(1313224) OTHER INFORMATION: n equals a, LOCATION: (1349473)..(1349473) OTHER INFORMATION: n equals a, LOCATION: (1349491)..(1349491) OTHER INFORMATION: n equals a, LOCATION: (1470091)..(1470091) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (1569020)..(1569020) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (1603734)..(1603734) OTHER INFORMATION: n equals a, NAME/KEY: misc\_feature\_LOCATION: (1637998) ..(1637998) OTHER INFORMATION: n equals a, LOCATION: (1602912)..(1602912) OTHER INFORMATION: n equals a, NAME/KEY: misc feature NAME/KEY: misc\_feature LOCATION: (1470091)..(1470091) 26; Conservative NAME/KEY: misc feature LOCATION: (779676)..(77 NAME/KEY: misc\_feature feature NAME/KEY: misc\_feature NAME/KEY: misc RESULT 2 US-09-328-352-642 Matches OTHER Ор ò DP

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Gaps

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70; DB 3;

Length 934;

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24.1%; Score 25.8; Di
Best Local Similarity 22.3%; Pred. No. 13;
Matches 23; Conservative 10; Mismatches
                                             NAME/KEY: CDS
LOCATION: 260..832
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Damagnez, Veronique
Smith, Susan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-838-973B-5/c; Sequence 5, Application US/08838973B; Patent No. 6277564; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 934 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 617-832-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Berlin, Vivian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: 260..832
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STRANDEDNESS: both
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Best Local Similarity 22.3
Matches 23; Conservative
    MOLECULE TYPE: CDNA
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                           FEATURE
                                                                                                             US-08-842-306B-5
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                  APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
FULD REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: ASSAYS AND REAGENTS FOR IDENTIFYING ANTI-FUNGAL AGENTS, AND USES RELATED THERETO
                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                                                                                                                                                                              24.3%; Score 26; DB 4; Length 318; 26.2%; Pred. No. 9.5;
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                                                                                                                                                                                                                                                                                                                                                         52;
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CURRENT APPLICATION DATA:
APPLICATION NDAER: US/08/842,306B
FILING DATE: 23-Apr-1997
PRIOR APPLICATION DATA:
APPLICATION NTMBER: US 08/771,212
FILING DATE: 20-DEC-1996
APPLICATION NUMBER: US 08/631,319
FILING DATE: 11-APR-1996
ATTOREY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-074.04
                                                                                                                                                                                                                                                                                                                                                      10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HOAG & ELIOT LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: One Post Office Square CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 UUNAGNNNNNNNNNNNAGAAAU 84
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Smith, Susan
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TELEPHONE: 617-832-1000
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Sequence 5, Application US/08842306B
Patent No. 6271197
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 934 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Berlin, Vivian
Levin, David
Ohya, Yoshikazu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FELEFAX: 617-832-7000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 5
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ADDRESSEE: FOLEY,
                                                                                                                                                                                                                                                                                                                                                         22; Conservative
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                                                                                                                                                                                                                                                                                                                                  Similarity
SENERAL INFORMATION:
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                                                                                                                                                                                                                                                                  IS-09-328-352-642
                                                                                                                                                                            SEQ ID NO 642
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Best Local S
Matches 22
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TITLE OF INVENTION: ASSAYS AND REAGENTS FOR IDENTIFYING ANTI-FUNGAL AGENTS, AND USES RELATED THERETO
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                                              183 AGTGAAAACTAAAGTAAAATAACAATAAAAATAGATTTAGGA 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,973B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.1%; Score 25.8; DB 3; 22.3%; Pred. No. 13; iive 10; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-074.05
                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 23-Apr-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/631,319
FILING DATE: 10-APR-1996
ATTORNEY/AGENT INFORMATION:
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us-09-646-651c-2.rni

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423 GCATAACCTGCATCATAGGCTGTCTTGCTTAGCTGCAAGAATAATGAAAATATTCTACC 364
         1 GGAAAAUNNINNINNINAUAUGINNINNINCUNNINTUUUNNINNAAAAANUANAAACAUNINNINC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 AAAAUINNNNUNAUAUGINNNNNNNNUUUUNNNNNNAAAAANUANAAAACAUNNNNNNCUU
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                                                                                     61 UUNAGNINNINNINNINNINAGAAAUININNINNINNINNINNINNINNINUUAGC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51; Indels
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APPLICANT: Wang, Tongtong
APPLICANT: Hosken, Ungun
APPLICANT: Hosken, Nancy A.

APPLICANT: Hosken, Mancy A.

APPLICANT: Hosken, Mancy A.

APPLICANT: Ralos, Michael D.

APPLICANT: Fanger, Gary R.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAP:

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAP:

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.45566

CURRENT APPLICATION NUMBER: US/09/480, 884A

CURRENT PLING DATE: 2001-08-27

NUMBER OF SEQ ID NOS: 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MoNeill, Patricia D.
VENTION: COMPOSITIONS AND METHODS FOR VENTION: AND DIAGNOSIS OF LUNG CANCER NCE: 210121.455C11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 24,6;
Pred. No. 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
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                                                                                                                                                                                                                   Sequence 126, Application US/09643597
Patent No. 6426072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Henderson, Robert A.
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27.2%;
                                                                                                                                                                                                                                                                                                                      Kalos, Michael D.
Bangur, Chaitanya
Hosken, Nancy
                                                                                                                                                                                                                                                                                                                                                                                                    Li, Samuel X.
Wang, Aijun
Skeiky, Yasir A.W.
                                                                                                                                                                                                                                                                                                                                                                                  Fanger, Gary R.
Li, Samuel X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 27.2 Matches 22; Conservative
                                                                                                                                                                                                                                                                                   Wang, Tongtong
Fan, Ligun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                               GENERAL INFORMATION: APPLICANT: Wang, T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -09-480-884A-126
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APPLICANT: Smith, S.
TITLE OF INVENTION: NUCLEIC ACIDS FOR IDENTIFYING ANTI-FUNGAL AGENTS, AND USES RELATE
TITLE OF INVENTION: THERETO
TITLE OF INVENTION: THERETO
CURRENT APPLICATION NUMBER: US/08/771,212A
CURRENT FILING DATE: 1996-12-20
PRIOR APPLICATION NUMBER: 08/631,319
PRIOR FILING DATE: 1996-04-10
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin version 3.1
SEQ ID NOS: 42
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                                   4 AAAUNININININAUAUGINININININCUINININININININAAAAANUANAAACAUININININCUUN 63
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                                                                           183 AGTGAAAACTAAAGTAAAATAACAATAAAAATAGATTTAGGA 141
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APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Glocat, S.
APPLICANT: Glocato, J.Y.
TITLE OF INVENTION: BSTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72;
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21.9%; Pred. No. 27;
tive 10; Mismatches
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Pred. No. 13
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Patent No. 6639063
                                                                                                                                                                                                                 Sequence 5, Application US/08771212A Patent No. 6455281
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ORGANISM: Candida sp
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Best Local Similarity
Matches 23; Conserv
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Best Local Similarity
Matches 23; Conserv
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OTHER INFORMATION:
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LENGTH: 499
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                                                                                                                                                                                  3 AAAAUNNINNUNAUAUGUKNINNINCUNNINUUUNNINNINAAAAANUANAAACAUNNINNCUU 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 AAAAUNINNNUNAUAUGUNNNNNNCUNNNNNNNAAAAANUANAAAACAUNINNNCUU 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
TITLE REPERENCE: 210121.45525
CURRENT APPLICATION NUMBER: US/09/221,107
CURRENT FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 161
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 126
LENGTH: 3552
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                                                                                                Score 24.6; DB 4; Length 3552;
Pred. No. 38;
8; Mismatches 51; Indels 0
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                                                                                                                                                                                                                                                                                                          3141 GAGTATCACTATGTGAAGAAA 3161
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; Patent No. 6660838
; GENERAL INFORMATION:
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PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 181
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                                                                                              Query Match 23.0%;
Best Local Similarity 27.2%;
Matches 22; Conservative
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APPLICANT: Cassell, Gail H.
APPLICANT: Chen, Ellson Y.
APPLICANT: Glass, Jennifer S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heiner, Cheryl R.
Lefkowitz, Elliot
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                     TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 22; Conserva
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                                              US-09-606-421B-126
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US-09-601-198-75/c
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US-09-221-107-126
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LENGTH: 3552
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APPLICANT:
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FEATURE: OTHER INFORMATION: chemically treated genomic
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INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 5614 base pairs
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STRANDEDNESS: double
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Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                  13 UNAUAUGUNINININCUNININUUUUNININAAAAANUAINAAAACAUNINININCUUNAGININININ 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Madeline Joy
APPLICANT: Stolk, John B.
APPLICANT: ALTOR B.
APPLICANT: A
                                                                                                                                                                                                              3 AAAAUNNININUNAUAUGINNINININCUNNINUUUNNININNAAAAANUANAAAACAUNNININCUU
                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                         353 ATCTAAAACGTCAATCAGACATTAATTCTAAATGAACATTAGAAG 309
                                                                                                                                              72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                           DB 4;
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STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                         ; Pred. No. 42;
11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 24.4; DE
Pred. No. 30;
9; Mismatches
                                                                   23.0%; Score 24.6; 21.0%; Pred. No. 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/401,064
CURRENT FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 371
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 398
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Patent No. 6623923
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1 Similarity 23.2%;
22; Conservative
                                                                                                                                       22; Conservative
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ORGANISM: Homo sapien
                                                                                                 Best Local Similarity
Matches 22; Conserv
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Best Local Similarity
Matches 22; Conserv
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US-09-601-198-75
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                                                                       Query Match
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Sequence 77, Application US/10204708

Patent No. 667731

GENERAL INPORMATION:

APPLICANT: DIEK Alexander

TITLE OF INVENTION: DY ASSESSING DNA Methylation

FILE REFERENCE: 5013.1012

CURRENT APPLICATION NUMBER: DO10-06-06

PRIOR APPLICATION NUMBER: DE 10019058.8

PRIOR APPLICATION NUMBER: DE 10019058.8

PRIOR PRILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-07

PRIOR FILING DATE: 2000-06-01

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 98

SEQ DID NOS: 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 5614;
              Diskette, 3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1492 AGCCTTAATATTGCGTGAAATATAATAAATAAATGATATA 1453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
MEDLUM TYPE: Diskette, 3.50 inch, 1.4M COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/956,171E FILING DATE: 20-Oct-1997 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
22.8%; Score 24.4; I
Best Local Similarity 22.0%; Pred. No. 48;
Matches 22; Conservative 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 99:
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0;

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JS-10-204-708-77
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0; Gaps Query Match 22.8%; Score 24.4; DB 4; Length 5915; Best Local Similarity 19.0%; Pred. No. 48; Matches 19; Conservative 12; Mismatches 69; Indels 0;

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3518 TGGTGGTAGGCGTTTGTAGTTATACGGGAGGTG 3557

Search completed: March 8, 2004, 06:01:49
Job time : 65 secs

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(without alignments)
320.775 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:+
| cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:+
| cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:+
| cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:+
| cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:+
| cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:+
| cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:+
| cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:+
| cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:+
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2421054 seqs, 1828716029 residues
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                                                                                                                                                                                      M nucleic - nucleic search, using sw model
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107
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

	Description		Sequence 280, App	GENERAL INFORMATI	Semional INFORMALI	Seguence 413, App	0000	Sometice 239, App	Sequence ilbs, Ap	Seguence 2, Appli	Semience 323248,	Semience gode	sociation and Apr	Sequence 1838, Ap	Sequence 1/808, A	Sequence 1, Appli Sequence 85840, A
SUMMARIES	ID	US-10-012-697-280	US-10-012-697-493	US-10-012-697-418	US-10-012-697-415	US-10-012-697-1307	US-10-311-455-239	US-10-311-455-1166		_	US-10-027-632-324208	US-10-027-632-8286	US-10-311-455-1858	118-09-814-353-17909	US-10-312-841-1	US-10-424-599-85840
		15	15	15	15	15	14	14	14	15	15	15	14	C	1 4	12
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	Query Match	25.6	25.6	25.6	25.6	25.6	25.0	25.0	25.0	24.9	24.9	24.9	24.9	24.5	24.5	24.3
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US-10-221-61	14 US-10-311-455-2062	4 US-10-312-841-	9-560-863-9	5 US-10-027-632-2	US-09-945-249-5	4 US-10-093-524	2 US-10-282-12	US-10-081-051-59	-10-282-122A-	4 US-10-081-051-58	US-09-764-860-1	US-09-764-904-91	4 US-10-091-548	4 US-10-074-095-113	5 US-10-212-872-1	US-09-908-711-158	US-09-764-860-11	US-09-764-877-264	US-09-860-670-232	US-09-764-904-90	0 US-09-764-891-	0 US-09-764-891-1	0 US-09-764-891-101	4 US-10-091-548-90	4 US-10-074-095-1	5 TIS-10-212-872-113	5 TIS-10-074-004-600	0-170-170 01 00 0	00-10-22/-646-232	5 US-10-242-515-2645
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## ALIGNMENTS

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NAME/KEY: misc_feature
LOCATION: 479, 484, 486, 487, 496, 501, 505, 506, 509, 511, 513, 514,
                                                                                                                                                                                                                                                                                                                         APPLICANT: Garcia, Veronica
APPLICANT: Jones, Lee William
TIPLICANT: Stache-Crain, Birgia
TITLE OF INVENTION: HUMAN GENES AND GENE EXPRESSION PRODUCTS
TITLE OF INVENTION: ISOLATED FROM HUMAN PROSTATE
FILE REPERENCE: 2300-16252
CURRENT APPLICATION NUMBER: US/10/012,697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/254,648
PRIOR FILING DATE: 2000-12-07
PRIOR FILING DATE: 2000-12-07
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 1568
SOFTHARE: FastSEQ for Windows Version 4.0
LENGTH: 524
Application US/10012697
5. US20030215803A1
                                                        APPLICANT: Escobedo, Jaime
APPLICANT: Garcia, Pablo Dominguez
APPLICANT: Kassam, Altaf
APPLICANT: Lamson, George
APPLICANT: Lamson, George
                                                                                                                                                                       Drmanac, Radoje
Crkvenjakov, Radon
Dickson, Mark
Drmanac, Snezana
Labat, Ivan
                                                                                                                                                                                                                                                                                     Leshkowitz, Dena
Kita, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                  Publication No. US20
GENERAL INFORMATION:
                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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748,

744,

736,

744, 748,

736,

FEATURE:

748,

744,

736,

744, 748

736,

0

Length 769;

25.6%; Score 27.4; DB 15; 24.3%; Pred. No. 1.4e+02;

Query Match Best Local Similarity

TYPE: DNA ORGANISM: Homo sapiens FEATURE:

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2 GAAAAUNNINININUAUAUGININININCUNININUUNININIAAAAANUANAAACAUNINININCU 61
                        misc_feature
534, 596, 615, 633, 641, 648, 656, 710, 729, 736, 744, 748,
749, 751, 752
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APPLICANT: Garcia, Veronica
APPLICANT: Jones, Lee William
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Birgit
TITLE OF INVENTION: HUMAN GENEE AND GENE EXPRESSION PRODUCTS
TITLE OF INVENTION: HOMAN GENES AND GENE EXPRESSION PRODUCTS
TITLE OF INVENTION: 1300-16252
CURRENT APPLICATION NUMBER: US/10/012,697
CURRENT FILING DATE: 2003-01-21
PRIOR PILING DATE: 2003-01-21
PRIOR PILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 1568
SOFTWARE: FastSEQ for Windows Version 4.0
US-10-012-697-418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69; Indels
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                                                                                                                                                         729.
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Pred. No. 1.4e+02;
9; Mismatches 69;
                                                                                                                                                       710,
                                                                                                                                                                                                                                                                 648, 656, 710,
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                                                                                                                                                     648, 656,
                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: misc feature
LOCATION: 534, 596, 615, 633, 641,
LOCATION: 749, 751, 752,
OTHER INFORMATION: n = A,T,C or G
                                                                                                                      NAME/KEY: misc_feature
LOCATION: 534, 596, 615, 633, 641,
LOCATION: 749, 751, 752
OTHER INFORMATION: n = A,T,C or G
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LOCATION: 534, 596, 615, 633, 641,
LOCATION: 749, 751, 752
OTHER INFORMATION: n = A,T,C or G
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LOCATION: 534, 596, 615, 633, 641,
LOCATION: 749, 751, 752
OTHER INFORMATION: n = A,T,C or G
                                                                                   OTHER INFORMATION: n = A, T, C or G
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Drmanac, Radoje
Crkvenjakov, Radomir
Dickson, Mark
Drmanac, Snezana
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Kita, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 24.3;
Matches 25, Conservative
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GAAAAUNNINNINNINAUAUGINNINNINNINUUUUNNINNINAAAAANUANAAACAUNNINNICU 61
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// LOCATION: 479, 484, 486, 487, 496, 501, 505, 506, 509, 511, 513, 514,

// LOCATION: 515, 516, 521, 523

// OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                            514,
                                                                                              501, 505, 506, 509, 511, 513, 514
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APPLICANT: Garcia, Veronica
APPLICANT: Jones, Lee William
APPLICANT: Stache-Crain, Birgit
TITLE OF INVENTION: HUMAN GENEE EXPRESSION PRODUCTS
TITLE OF INVENTION: 1SOLATED FROM HUMAN PROSTATE
TITLE OF INVENTION: 1SOLATED FROM HUMAN PROSTATE
FILE REFERENCE: 2300-16252
CURRENT APPLICATION NUMBER: 0S/10/012,697
FRIOR FILING DATE: 2000-12-07
PRIOR PRILOR APPLICATION NUMBER: 60/254,648
PRIOR FILING DATE: 2000-12-07
PRIOR FILING DATE: 2000-03-13
NUMBER OF SEQ ID NOS: 1568
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 25.6%; Score 27.4; DB 15; Length 524; Best Local Similarity 24.3%; Pred. No. 1.2e+02; Matches 25; Conservative 9; Mismatches 69; Indels 0
                                                                                                                                                                                                          511,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              292 TCAGTAAAAACACTTTTAGAGATTGTGTTTCCTTTTTTGTGAG 334
                                                                                                                                                                                                                                                                                                                 509,
                                                                                                                                                                                                          509,
                                                                                                                                                                                                       506,
                                                                                                                                                                                                                                                                                                                 505, 506,
                                                                                                                                                                                                     505,
                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 479, 484, 486, 487, 496, 501,
LOCATION: 515, 516, 521, 523
OTHER INFORMATION: n = A,T,C or G
FEATURE:
                                                                                                                                                                                                     501,
                                                               NAME/KEY: misc feature
LOCATION: 479, 484, 486, 487, 496,
LOCATION: 515, 516, 521, 523
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 479, 484, 486, 487, 496,
LOCATION: 515, 516, 521, 523
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3-10-012-697-493
Sequence 493, Application US/10012697
Publication No. US20030215803A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Garcia, Pablo Dominguez
Kassam, Altaf
Lamson, George
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scott, Beth
Drmanac, Radoje
Crkvenjakov, Radomir
Dickson, Mark
Drmanac, Snezana
LOCATION: 515, 516, 521, 523
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drmanac, Snezana
Labat, Ivan
Leshkowitz, Dena
Kita, David
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APPLICANT: Escobedo, Jaime
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APPLICANT: APPLICANT:

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2 GAAAAUNNNNNNUAUAUGNNNNNNCUNNNNUUUNNNNNAAAAANUANAAACAUNNNNNCU 61
                                                                 Gaps
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928
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928
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LOCATION: 649, 785, 791, 795, 806, 818, 855, 858, 869, 882, 912,
LOCATION: 919, 920, 921, 923, 926, 927, 928
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   855, 858, 869, 882, 912,
928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Garcia, Veronica
APPLICANT: Garcia, Veronica
APPLICANT: Jones, Lee William
APPLICANT: Stacche-Crain, Birgit
TITLE OF INVENTION: HUMAN GENES AND GENE EXPRESSION PRODUCTS
TITLE OF INVENTION: HUMAN GENES AND GENE EXPRESSION PRODUCTS
TITLE OF INVENTION: HUMAN GENES AND GENE EXPRESSION PRODUCTS
TITLE OF INVENTION: HUMAN GENES AND GENE EXPRESSION PRODUCTS
TITLE OF INVENTION: HOMENE: US/10/012,697
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: 60/254,648
PRIOR APPLICATION NUMBER: 60/254,648
PRIOR APPLICATION NUMBER: 60/255,668
PRIOR APPLICATION NUMBER: 60/255,668
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 1568
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 1307
             Score 27.4; DB 15; Length 789;
Pred. No. 1.4e+02;
9; Mismatches 69; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        882,
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928
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927,
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927,
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927,
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                                                                                                                                                                                                                                                                                                                                                      Sequence 1307, Application US/10012697
Publication No. US20030215803A1
                                                                                                                                                                                                                                                                                                                                                                                                                                              Garcia, Pablo Dominguez
Kassam, Altaf
Lamson, George
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LOCATION: 649, 785, 791, 795, 806,
LOCATION: 919, 920, 921, 923, 926,
OTHER INFORMATION: n = A,T,C or G
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LOCATION: 649, 785, 791, 795, 806,
LOCATION: 919, 920, 921, 923, 926,
OTHER INFORMATION: n = A,T,C or G
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LOCATION: 649, 7485, 791, 795, 806,
LOCATION: 919, 920, 921, 923, 926,
OTHER INFORMATION: n = A,T,C or G
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LOCATION: 649, 785, 791, 795, 806,
LOCATION: 919, 920, 921, 923, 926,
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drmanac, Radoje
Crkvenjakov, Radomir
Dickson, Mark
Drmanac, Snezana
             25.6%;
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Leshkowitz, Dena
Kita, David
         Query Match
Best Local Similarity 24.33
Matches 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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APPLICANT:
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NAME/KEY: misc_feature
LOCATION: 5, 7, 9, 12, 15, 17, 19, 20, 27, 33, 46, 62, 63, 64, 66,
LOCATION: 67, 74, 76, 509, 613, 645, 651, 655, 666, 678, 715, 718, 729, 742, 772,
OTHER INFORMATION: n = A,T,C or G
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LOCATION: 5, 7, 9, 12, 15, 17, 19, 20, 27, 33, 46, 62, 63, 64, 66,
LOCATION: 67, 74, 76, 509, 613, 645, 651, 655, 666, 678, 715, 718, 729, 742, 772,
OTHER INFORMATION: n = A,T,C or G
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LOCATION: 5, 7, 9, 12, 15, 17, 19, 20, 27, 33, 46, 62, 63, 64, 66,
LOCATION: 67, 74, 76, 509, 613, 645, 651, 655, 666, 678, 715, 718, 729, 742,
OTHER INFORMATION: n = A,T,C or G
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LOCATION: 5, 7, 9, 12, 15, 17, 19, 20, 27, 33, 46, 62, 63, 64, 66,
LOCATION: 67, 74, 76, 599, 613, 645, 651, 655, 666, 678, 715, 718, 729, 742,
OTHER INFORMATION: n = A,T,C or G
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LOCATION: 5, 7, 9, 12, 15, 17, 19, 20, 27, 33, 46, 62, 63, 64, 66,
LOCATION: 67, 74, 76, 509, 613, 645, 651, 655, 666, 678, 715, 718, 729,
OTHER INFORMATION: n = A,T,C or G
                                         2 GAAAAUNINININININAUAUGINININININUUUUNININININAAAAANUANAAACAUNINININCU
         0; Gaps
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APPLICANT: Leshkowitz, Dena
APPLICANT: Leshkowitz, Dena
APPLICANT: Kita, David
APPLICANT: Garcia, Veronica
APPLICANT: Jones, Lee William
APPLICANT: Stache-Crain, Birgia
III.B. OF INVENTION: HUMAN GENES AND GENE EXPRESSION PRODUCTS
TITLE OF INVENTION: ISOLATED FROM HUMAN PROSTATE
      69; Indels
                                                                                                                                                                            148 TCAGTAAAACACTTTTAGAGATTGTGTTTCCTTTTTTGTGAG 190
                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 2300-16252
CURRENT APPLICATION NUMBER: US/10/012,697
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: 60/254,648
PRIOR FILING DATE: 2000-12-07
PRIOR FILING DATE: 2000-13-07
PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 1568
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 349
                                                                                                                                                                                                                                                                                           Sequence 415, Application US/10012697
Publication No. US20030215803A1
GENERAL INFORMATION:
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APPLICANT: Garcia, Pablo Dominguez
APPLICANT: Kassam, Altaf
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Crkvenjakov, Radomir
Dickson, Mark
Drmanac, Snezana
25; Conservative
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Scott, Beth
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ORGANISM: Homo sapiens
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APPLICANT:
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Matches
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GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
FILE REFERENCE: E01/1208/WO
CURRENT ARPLICATION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
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Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3673778;
                                                                                                                                                                                                            OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                                                                                                                                      25.0%; Score 26.8; DB 14; Length 13814; 22.1%; Pred. No. 5.9e+02; ive 11; Mismatches 70; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Mismatches
                   PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
                                                                                                                                                                                                                                                                                       ; LOCATION: 9297
; CTHER INFORMATION: n is a or g or c or
US-10-311-455-1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/10312841
Publication No. US20030186277A1
                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                      23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 23; Conserv
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Best Local Similarity
Matches 23; Conserv
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US-10-027-632-323248/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (379615)
US-10-312-841-2
                                                                                                                                                                                                                                                                 NAME/KEY: unsure
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                                                                                            SEQ ID NO 1166
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                           FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Publication No. Ug20030143606A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: OLENGEN OF DISCASSES ASSOCIATED With the Immune System by Determ
ITILE OF INVENTION: Oytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER: OF SEQ ID NOS: 2424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1166, Application US/10311455
Publication No US20030143606A1
GENERAL INFORMATION:
APPLICANT: DIEX, Alexander
APPLICANT: BIEPENBROCK, Christian
APPLICANT: BIEPENBROCK, Christian
APPLICANT: BIEPENIN, Wirt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detern
TITLE OF INVENTION: cytosine methylation
TITLE OF INVENTION: Cytosine methylation
CURRENT APPLICATION NUMBER: US/10/311, 455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 25.0%; Score 26.8; DB 14; Length 6419; Best Local Similarity 24.0%; Pred. No. 4.4e+02; Matches 25; Conservative 9; Mismatches 70; Indels 0;
                                                      Score 27.4; DB 15; Length 929;
Pred. No. 1.5e+02;
9; Mismatches 69; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1212 AAAAAACAACCTACCCAAAAATCACCCAACAAACTATTCTAACA 1169
                                                                                                           69; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 239, Application US/10311455
                                               Query Match
Best Local Similarity 24.3%;
Matches 25; Conservative
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US-10-012-697-1307
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LENGTH: 6419
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TYPE: DNA

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Sequence 1858, Application US/10311455
Publication No. US2003014360641
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PERENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: cytosine methylation
TITLE OF INVENTION: cytosine methylation
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EF01/07537
PRIOR APPLICATION UNMBER: DE 10032529.7
                                                                             421 GGAAGAGACCATTCTTTGCATACCCCATTTTCTGGATAAAAAGAAAAAGACATTCCTGT 480
                         3 AAAAUNNNNUNAUAUAUGNNNNNNNUUUNNNNNNNNAAAAANUANAAACAUNNNNNCUU 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INCHARATION:

APPLICANT: Wang, David G.

TITLE OF INVERTION: Telefitication and Mapping of Single Nucleotide

TITLE OF INVERTION: Polymorphisms in the Human Genome

FILE REPERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-04-20

PRIOR PRIOR DATE: 2000-04-20

PRIOR PRIOR DATE: 2000-04-20

PRIOR PLING DATE: 2000-03-24

PRIOR FILING DATE: 2000-03-24

PRIOR FILING DATE: 2000-02-24

PRIOR FILING DATE: 1999-11-23

PRIOR PILING DATE: 1999-11-23

PRIOR PILING DATE: 1999-109-28

PRIOR PILING DATE: 1999-09-28

PRIOR PILING DATE: 1999-09-38

PRIOR PILING DATE: 1999-09-38
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481 TTTGATCTTTTAATTCAAGAATGGGGGCAAAACCAACCTAATČTĞ 527
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                                                                                                                                                                                                                                    318 AAGTTACCAGAATGTGCATAATCATTACTTCATGATCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.9%; Score 26.6; DB 15; 23.4%; Pred. No. 2.2e+02;
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FILING DATE: 2000-06-30
APPLICATION NUMBER: DE 10043826.1
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8286, Application US/10027632
Publication No. US20030204075A9
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Matches 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-027-632-8286
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Publication No. US2033020407549
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT FILING DATE: 2002-04-30
PRIOR PLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PLICATION NUMBER: US 60/198,676
PRIOR PELICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-04-20
PRIOR PELING DATE: 2000-04-20
PRIOR PELING DATE: 2000-03-29
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-08-09
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                         PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PLING DATE: 2000-07-12
PRIOR PLING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR PRILORION NUMBER: US 60/185,218
PRIOR PRILORION NUMBER: US 60/185,218
PRIOR PRILORION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PRILOR DATE: 1999-09-28
PRIOR PRILOR DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-09-09-09
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SOFTWARE: FastSEQ for Windows Version 4.0
NT FILING DATE: 2002-04-30
APPLICATION NUMBER: US 60/218,006
APPLICATION NUMBER: US 60/198,676
APPLICATION NUMBER: US 60/198,676
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Best Local Similarity
Matches 22; Conserv
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ORGANISM: Human
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SEQ ID NO 324208
LENGTH: 488
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Length 634;

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Publication No. US20030165831A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Limin, James

TITLE OF INVENTION:

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                                                                                                                                                                                                                                                                                                                                                              24.9%; Score 26.6; DB 14; Length 10034; 17.2%; Pred. No. 6e+02; Live 15; Mismatches 67; Indels 0;
                                                                                                                                                                                                                                                       ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-1858
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17808
LENGTH: 390
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                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Best Local Similarity 23.5%
Matches 19; Conservative
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Best Local Similarity
....hes 17; Conserva
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US-09-814-353-17808
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                                                                                                                  10034
                                                                         SEQ ID NO 1858
LENGTH: 1003
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; Sequence 1, Application US/10312841

RESULT 14 US-10-312-841-1/c

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APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MH(
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MH(
CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
LENGTH: 3673778
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thous A
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Caro Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
EENGTH: 511
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24.5%; Score 26.2; DB 14; Length 3673778;
Best Local Similarity 22.9%; Pred, No. 9.4e+02;
Matches 24; Conservative 10; Mismatches 71; Indels 0; G
                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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24.3%; Score 26; DB 12; Length 511;
Best Local Similarity 24.0%; Pred. No. 3e+02;
Matches 24; Conservative 8; Mismatches 68; Indels
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US-10-424-599-85840
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Publication No. US20040031072A1
GENERAL INFORMATION:
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LOCATION: (3294164)
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Publication No. US20
GENERAL INFORMATION:
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US-10-312-841-1
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679 bp DNA linear GSS 09-OCT-2002
B.oleracea002 Brassica oleracea genomic, genomic survey
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Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T., Nash, W., Rabinow.cz, P.D. and Wilson, R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
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Seg primer: -21UPpOT forward
Class: shotgun
High quality sequence start: 17
High quality sequence stop: 551.
        CNS057N6
AQ135026
AQ205663
                                  AQ268612
AQ211558
AL915410
AL915411
BH719067
BH654909
                                                                                        CBO50688
CBO50532
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BX684795 BX684795
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                                                      8, 2004, 04:24:32; Search time 2381 Seconds (without alignments) 1341.980 Million cell updates/sec
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   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                     nucleic search, using sw model
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Listing first 45 summaries
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BZ262911

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CF259384 CC077740

AG008606

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Tissue Procurement: David N. Louis, M.D.
CDNA library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The T.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to:
Seq primer: -40UP from Gibco
High quality sequence stop: 421.
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                                                                                                                                        flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."
                                                                                                                                                                                                                                                                                                                                                                                                                              333 AAAATTACATAGATATTACCTCTAGATTTGTTTAAAAAATTATTAAAATCTTTACTA 274
                                                                                                                              genome shotgun library from
                                                                                                                                                                                                                                                                                                                                                                                        3 AAAAUNNNNUNAUAUGUNNNNNNCUNNNUUUNNNNNAAAAANUANAAACAUNNNNNCUU 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 453)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological CGAP/BTGAP); Tumor Genome Anatomy Project
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DH108 (TI phage resistant)"
/clone lib="NCI CGAP Brn65"
/note="Organ: brain; "Vector: pCMV-SPORT6; Site 1: NotI; Site 2: Sali; Cloned unidirectionally, Primer: Oligo dr. Average insert size 1.77 kb. Constructed by Life
                                                                                                                                                                                                                                                                                                                                                           Gaps
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|tissue_type="glioblastoma without EGFR amplification"
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                                                                                                                                                                                                                                                                                                                   Length 679;
                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      273 AATCGTTTACAACCTCAAAATCTCAGAATCGGCGGAAGTAG 232
                                                                                                                                                                                                                                                                                                            ; Score 29.6; DB 28;
; Pred. No. 1.1e+03;
11; Mismatches 67;
                                          organism="Brassica oleracea"
                                                          /mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.oleracea002"
/note="Vector: pOTw13; Whole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
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/db_xref="taxon:9606"
    ocation/Qualifiers
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23.58;
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Matches 24; Conservative
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                                                                                             This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
CDNA was oligo dT primed from 5ug of poly A+ RNA from neurula.
BCORI-NOLI cut cDNA was then ligated into pCS107 with EcoRI at the 5, end and NoLI at the 3' end.
Vector: pCS107; Site 1: EcoRI; Site 2: NotI
Host: Escherichia coli DH10B.
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/clone_lib="XGGC_neurula"
/note="Vector: pCS107; Site_1: EcoRI, Site_2: NotI; cDNA
was oligo dT primed from Sug of poly A+ RNĀ from neurula.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end."
                                                                                                                                                                                                                                                                                                                                                                                                                                    Silurana tropicalis (western clawed frog)
Silurana tropicalis
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Taylor, R., Zorn, A.M. a. project 2001 (11_2003)
                          Indels
                                                                                                                                              249 ACAAGITITATATCIGAGAAAAAAAAAGGAAIGAITCCAITA 291
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                      68;
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/lab_host="Escherichia_coli_DH10B"
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المام عليان
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TROPICALIS_SEQUENCE ID: INeu075020.glkT7
Sequencing primer: T7
    Pred. No. 1.7e+03;
11; Mismatches 68
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Croning,M.D.R., Ashurst,J.L.,
Sanger Kenopus tropicalis EST
Unpublished (2003)
Contact: Croning MDR
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/db_xref="taxon:8364"
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Email: trop@sanger.ac.uk
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23.3%;
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Thes 26; Conservative
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RESULT 4 BH488315

Length 453;

DB 10;

27.1%; Score 29;

Query Match

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Query Match
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       GSS 13-DEC-2001
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                                                                                                                                               Embryophyta; Tracheophyta;
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BOGKAS7TR BOGK Brassica oleracea genomic clone BOGKA57, genomic
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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BH488315
BOGWD90TF BOGW Brassica oleracea genomic clone BOGWD90, genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone lib="BOGW"
/note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstX1 linkers"
                                                                                                                    Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 685)
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
Other_GSSs: BOGKAS7TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 685;
                                                                                                                                                                                                                                                                                                                                                      Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Brassica oleracea"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="TO1000DH3"
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Location/Qualifiers
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BH488315.1 GI:17696419
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Fax: 301-838-0208
Email: cdtown@tigr.org
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Fax: 301-838-0208
Email: cdtown@tigr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26; Conservative
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                                                                                                       Brassica oleracea
                                     survey sequence.
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BH489963
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Matches 26; Conserv
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H489963/c
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UNSUS7N6 1125 bp DNA linear GSS 26-JUL-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 010KO4 of library A from Tetraodon nigroviridis, genomic survey sequence.
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BP 191 91006 BURY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

Web : www.genoscope.cns.fr)

This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

In .1125
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Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,
Tetradontoidea, Tetraodontidae, Tetraodon.
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| 128 GGAAAATATATATAAAGAATTTTTTTTATAGAATGAAAATTTCACACAAATTTTC
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Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Welssenbach, J.
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DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
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                                                                                                                                                                                                                                                                                                                                                                                                           26.9%; Score 28.8; DB 28;
24.5%; Pred. No. 1.5e+03;
tive 10; Mismatches 70;
                                                                                                                                       organism="Brassica oleracea"
                                                                                                                                                                /mol_type="genomic_DNA"
/strain="TO1000DH3"
                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
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                                                 Class: sheared ends
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HS_3053_A2_A11_MR CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3053 Col=22 Row=A, genomic survey
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Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                            247 AAAATAACTAAAATHTTTTAACTTGCATTTATATATATCAAAAGGATAAACTTTAACTCTT 188
                                                                                                                                                                                                                                                                       3 AAAAUNNNNNUNAUAUGUNNNNNNCUNNNNUUUUNNNNAAAAANUANAAAACAUNNNNNNCUU 62
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="010K04"
/clone_lib="A"
/note="Genoscope sequence ID : COAA010BF02C3~end : T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
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23.5%; Pred. No. 3.1e+03;
Live 10; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                               187 AGCTTTTATCAGATGAACAAGTGTATTTGAGGTCTGTTTA 147
                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="Plate=3053 Col=22 Row=A"
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/organism="Homo sapiens"
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Plate: 3053 row: A colu
Class: BAC ends
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AQ135026.1 GI:3526392
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Best Local Similarity 23.59
Matches 24; Conservative
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 394)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                        AQ205663

394 bp DNA linear GSS 17-SEP-1998
HS_3236_B2_A03_MR CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3236 Col=6 Row=B, genomic survey
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/note="Organ: Sperm; Vector: pBeloBAC11; BAC Clones in
5-Coli DH10B"
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Fax: (206) 616-3887
Email: Jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3236 row: B column: 6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 28; Length 394;
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293 TAÄGGTTTATAATGTGTÄÄÄGTAAAGTGTATTATAACCATÄ 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3236 Col=6 Row=B"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 26.2%; Score 28; DB 28; Similarity 23.5%; Pred. No. 3e+03; 24; Conservative 10; Mismatches 6
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Location/Qualifiers
                                                                                                                                                                                      AQ205663
AQ205663.1 GI:3616233
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GSS.
                                                                                                                                                                                                                                                    Homo sapiens (human)
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                                                                                                                                                                                                                                                                         Homo sapiens
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Best Local Similarity
Matches 24; Conserv
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ORGANISM
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LOCUS
DEFINITION
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AUTHORS
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PUBMED
COMMENT
                                                               RESULT 8
AQ205663
                                                                                                                                                                                      ACCESSION
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KEYWORDS
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KEYWORDS
SOURCE
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ORGANISM

EFERENCE AUTHORS TITLE JOURNAL JOMMENT

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AL915410
AL915410 PJR-Z1+Z2 Danio rerio cDNA clone 193-E07-1, mRNA sequence.
AL915410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopteryqii, Meopteryqii, Teleostei, Ostariophysi,
Cypriniformes; Cyprinidae, Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GAAAAUNNNNUNAUAUGUNNNNNNCUNNNNUUUNNNNNAAAAANUANAAAACAUNNNNNCU
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Nang,W., Weh,Z. and Peng,J.
15000 unique zebrafish EST clusters and their future use in microarray for profiling gene expression patterns during
High Throughput Sequencing Center
University of Washington
101 Queen Anne Avenue North, Seattle, WA 98109, USA
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101 Queen Anne Avenue North, Seattle, WA 98109, USA
102 Fax: (206) 616-3887
103 Fax: (206) 616-3887
103 Fax: (206) 616-3887
103 Fax: (200) 616-3887
103
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Lab Of Euctional Genomics
Institute of Molecular and Cell Biology
30 Medical Drive, Singapore, 117609, Singapore
Email: pengir@imcb.a-star.edu.sg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 UNAGNINININININININAGAAAUNINININININININININININI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="whole embryo or fish"
/dev_stage="mixed stages"
/clone_lib="PDR-Z1+Z2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="Plate=3235 Col=2 Row=J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone requests: pengir@imcb.a-star.edu.sg.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                              High quality sequence stop: 406
Location/Qualifiers
1. 406
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/strain="local wildtype"
/db_xref="taxon:7955"
/clone="193-E07-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Danio rerio"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 23.59 Matches 24; Conservative
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VERSION
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                                                                         Adams. M. D. Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Garager, D., Suh, B., Wible, C., de Jong, P. and Venter, J.C. Unpublished (1998)
Contact: Mark Adams
The Institute for Genomics
The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA
Fex. 301 838 0200
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Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSS 18-SEP-1998
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                            Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bmail: mdadams@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC

Library availability, please contact Pieter de Jong

(pieter@dejong med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

RACPAC Resources (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GAAAAUNINNINUNAUAUGININNINUCUNINNIUUUUNINNINAAAAANUANAAACAUNINNINCU 61
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HS_3235_B2_E01_MR_CIT_Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3235 Col=2 Row=J, genomic survey
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Contact: Mahairas GG, Wallace JC, Hood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic_DNA"
|db_xref="GDB:7527118"
|db_xref="taxon:9606"
|clone="RPCI-11-71J23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1. .394
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AQ211558
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Query Match

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BH654909 807 bp DNA linear GSS 19-FBB-2002 BOHTZ17TF BO_2_3_KB Brassica oleracea genomic clone BOHTZ17,
                                                                          Tracheophyta;
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genomic DNA inserted into pHOS1 using BstXI linkers"
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                        Brassica oleracea
Brassica oleracea
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheor
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brássica.
1 (bases 1 to 618)
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
                                                                                                                                                          and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spermatophyta; Magnoliophyta; eudicotyledons; core eudicorrosids; eurosids II; Brassicales; Brassicaceae; Brassica
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                                                                                                                                                                                                                                                                                                                                         Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seg primer: TF
Class: sheared ends.
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DNA is from a doubled haploid provided by Tom Osborn.
Sleg primer: IT
Sleg primer.
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                                                                                                                                                                                                                                                                                       MD 20850,
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Unpublished (2001)
Other GSSs: BOKKL74TR
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/organism="Brassica oleracea"
/mol type="genomic DNA"
/strain="TOl000DH3"
                                                                                                                                                                                                                                                                              9712 Medical Center Drive, Rockville,
Tel: 301-838-3523
Fax: 301-838-0208
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Tel: 301-838-3523
Fax: 301-838-0208
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BH654909.1 GI:18713150
GSS.
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JOURNAL
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AL915411 PJR-Z1+Z2 Danio rerio cDNA clone 192-E07-1, mRNA sequence.
AL915411
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BH719067.1 GI:18818288
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Cytinopterygii, Neopterygii, Teleostei, Ostariophysi,
Cypriniformes, Cyprinidae, Danio.
1 (bases 1 to 539)
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15000 unique zebrafish EST clusters and their future use in microarray for profiling gene expression patterns during
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          Score 27.8; DB 9; Length 539;
Pred. No. 2.9e+03;
8; Mismatches 70; Indels
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                                                  70; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Peng J
Lab of Functional Genomics
Institute of Molecular and Cell Biology
Institute of Molecular and Cell Biology
Medical Drive, Singapore, 117609, Singapore
Email: pengir@imcb.a-star.edu.sg
Clone requests: pengir@imcb.a-star.edu.sg.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:7955"
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/dev_stage="mixed stages"
/clone_lib="puR-Z1+Z2"
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embryogenesis Genome Res. 13 (3), 455-456 (2003)

12618376 22505427

JOURNAL MEDLINE PUBMED COMMENT

AL915411.1 GI:23180709 Danio rerio (zebrafish)

DEFINITION ACCESSION

RESULT 12

AL915411

LOCUS

Danio rerio

SOURCE ORGANISM

REFERENCE AUTHORS

TITLE

VERSION KEYWORDS

/organism="Danio rerio" /mol\_type="mRNA" /strain="local wildtype"

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FEATURES

Query Match
Best Local Similarity 25.7
Matches 27; Conservative

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DEFINITION

RESULT 13 BH719067 LOCUS ACCESSION

VERSION

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Query Match
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25.6%; Score 27.4; DB 14; Length 204;

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/dev stage="adult"
/lab host="DH10B"
/lab host="DH10B"
/clone lib="NGLGAP_Pr28"
/note="Organ: prostate; Vector: pT713D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NGLGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
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DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NGI-CGAP clone distribution information can be
info@image.llnl.gov
Plate: LLAM8010 row: D column: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204 bp mRNA linear BST 17-JAN-2003
NISC_gj19b02.y1 NCI_CGAP_Pr28 Home sapiens cDNA clone IMAGE:3272018
5', mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 204)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                    Gaps
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genomic DNA inserted into pHOS1 using BstXI linkers"
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564 AAAATTTAAAAATAGTTTAAATTTTATATGAATATAAATT
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19.0%; Pred. No. 2.8e+03;
iive 14; Mismatches 67;
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Seg primer: M13RP1 reverse primer (ABI).
'organism="Brassica oleracea"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation:
                      /mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
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Best Local Similarity 19.03
Matches 19; Conservative
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Unpublished (1997)
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